GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

March Run on:

7, 2006, 17:40:32 ; Search time 11.7198 Seconds (without alignments) 1087.222 Million cell updates/sec

US-09-938-406-1_COPY_523_551

Perfect score:

1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Geneseq 21:* Database

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp2000s:* geneseqp2001s:* geneseqp1990s: geneseqp2002s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

STIMMADIES

		*			SUMMARIES	
Result No.	Score	Query Match	, Length DB	DB	ID	Description
1	139	100.0	269	2	AAY22833	Aay22833 SEO ID NO
7	139	100.0	269	ß	ABG68304	
٣	139	100.0	269	9	ABU57711	_
4	139	100.0	649	~	AAW44250	Aaw44250 HIV-1 qp1
S	139	100.0	865	~	AAW43072	Aaw43072 HIV-1 qp1
9	131	94.2	699	ø	ABP73114	Abp73114 Amino aci
7	131	94.2	699	9	ABP73117	
დ	131	94.2	699	9	ABP73122	Abp73122 Amino aci
6	131	94.2	699	9	ABP73120	
10	131	94.2	844	9	ABP73115	Abp73115 Amino aci
11	131	94.2	844	9	ABP73112	Abp73112 Amino aci
12	131	94.2	844	9	ABP73118	Abp73118 Amino aci
13	131	94.2	844	9	ABP73121	
14	. 131	•	844	9	ABP73111	Abp73111 Amino aci
15	130	٠	791	σ	ADX39690	Adx39690 HIV Env p
16	130	93.5	883	4	AAB82761	Aab82761 Ancestral
17	130	93.5	883	თ	ADW38347	Adw38347 Ancestral
18	130	93.5	883	σ	ADY27998	Ady27998 HIV-1 gro
19	130	93.5	883	σ	AEB10654	
20	130	93.5	883	σ	AEB10552	Aeb10552 HIV-1, su
21	129	95.8	267	ď	AAY22831	Aay22831 SEQ ID NO
	129	92.8	267	Ŋ	ABG68302	Abg68302 Envelope
23	129	92.8	267	ø	ABU57709	Abu57709 Human imm
24	129	92.8	855	σ	ADX39676	Adx39676 HIV Env p

	SEO Enve Huma HIV-	Aay22836 SEQ ID NO Aay22848 SEQ ID NO Aay22829 SEQ ID NO Abc68300 Frvelone		Abu57714 Human imm Abr57596 HIV gp41 Adx39673 HIV Env p Adx33674 HIV Env p Aar12261 HIV-1 etr Aay22825 SEQ ID NO
AAY22851 ABG68322 ABUS7729	AAY22816 ABG68287 ABU57694 AAW43069	AAY22836 AAY22848 AAY22829 ABG68300	ABG68307 ABG68319 ABUS7707 ABUS7726	ABU57714 ABR57596 ADX39673 ADX39674 AAR12261 AAY22825
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25 26 27	330 310 310	9 9 9 9 2 2 2 4 4 7	3 3 3 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	4 4 4 4 4 4 0 1 2 E 4 2

ALIGNMENTS

RESULT 1

HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine; antibody; viral membrane fusion; viral infectivity; ligand affinity purification; protein A replacement; mmunoglobulin purification; epitope minic. AAY22833 standard; protein; 269 AA. SEQ ID NO. 29 from WO9820036. (first entry) 19-AUG-1999 AAY22833; AAY22833

Human immunodeficiency virus

WO9820036-A1.

14-MAY-1998.

97WO-US020069. 05-NOV-1997; 96US-00743698 97US-00876698 06-NOV-1996;

(GETH) GENENTECH INC

Starovasnik MA; Mcdowell RS, Phelan JC, Braisted A, Judice JK, Wells JA;

WPI; 1998-286866/25.

Production of constrained helical peptide(s) by linking side chains on termini of octa:peptide - derived from human immunodeficiency virus gp41 protein, useful in vaccines for treatment and prevention of infection.

Claim 11; Page 170; 279pp; English:

Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus (HIV). Specifically, AAY22810-Y22910 are derived from gr41 proteins of known HV virus strains (AAY22810, AAY22810, AAY2280, AAY22880, AAY22803 represent consensus sequences of various sections of the gp41 protein). Sequences derived from the peptides are used to produce constrained helical peptides of the invention. The constrained helical peptide is produced by synthesising an octapeptide in which both terminal amino acids have a side-chain that includes a group able to form an amide

of, HIV infection, either as antifusion/anti-infection agents or

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            residues with a difunctional linker to produce two amide bonds. The constrained helical peptides are used to treat or prevent HIV infection, especially as vaccines that generate antibodies that prevent wiral membrane fusion or infectivity. Vaccines may contain constrained helical peptides derived from several different strains of HIV. The antibodies are also useful for diagnosing HIV infection. Other uses for the constrained helical peptides are in affinity purification of ligands (particularly where complete binding protein is not readily available, e.g. replacements for protein A in immunoglobulin purification), as epitope mimics for antibody production; for isolation of synthetic antibody clones from phage display libraries, or as stable forms of
 and cyclising the octapeptide by reacting the specified side-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV; glycoprotein; gp41; antigen; helical conformation;
virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;
viral envelope protein; vaccine; virucide; anti-HIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Envelope protein gp41 from HIV clade B strain #23.
                                                                                                                                                                                                                                                                                     100.0%; Score 139; DB 2;
100.0%; Pred. No. 9.2e-11;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG68304 standard, protein; 269
                                                                                                                                                                                                                      "floppy" peptides or proteins
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(first entry)
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
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29; Conserv
                                                                                                                                                                                                                                                      Sequence 269 AA;
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07-OCT-2002
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preferably where associated with a carrier, as an immunogen (including as vaccine) to raise antibodies. The antibodies may be used for diagnosis or prevention/treatment of HIV infection (i.e. acquired immunodeficiency syndrome, AIDS), e.g. prevention of mother-to-child transmission or in cases of health care accidents. The peptides can be based on specific HIV strains, e.g. breakthrough isolates of HIV that have developed during vaccine trials, so a combination of them should cover a wide range of protection. The present sequence is gp41 protein from a particular HIV clade used to derive a consensus sequence of gp41. (Updated on 29-AUG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a constrained helical peptide compound (I) comprising a first constrained helical peptide comprising a sequence of 8 amino acids (a.as) having a first and second terminal residue both flanking an internal sequence of 6 a.as, where the terminal residues have a side chain that are linked to each other forming a locking group to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel constrained helical peptide compound useful for prophylactically or therapeutically treating mammal at risk for or infected with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus; HIV; vaccine; helical peptide compound; hapten; immunogen; peptidomimetic; gp41;
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus (HIV) envelope protein gp41 #23.
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; Pred. No. 9.2e-11;
0; Mismatches 0;
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97US-0049787P.
97US-00876698.
97US-00965056.
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100.0%;
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                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.'
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency viral membrane fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRAISTED A C.
JUDICE J K.
MCDOWELL R S.
PHELAN J C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          envelope protein.
                                                                                                                                                                                       Sequence 269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002151473-A1.
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cc antibodies that prevent viral membrane fusion, as haptens, preferably attached to a carrier, for use as an immunogen to raise antibodies that tached to a carrier, for use as an immunogen to raise attached to a carrier, for use as an immunogen to raise antibodies that cc attached to a carrier, for use as an immunogen to raise at risk of cc have a diagnostic use, as a vaccine for treatment of patients at risk of cor infected with HIV, to create combinatorial constrained helical peptide cc libraries that are useful in Chemical selection systems, to isolate the libraries for alpha-helical binding domains of known proteins, for determining whether a binding domains of known protein of proteins of peptidomimetics, to replace intact binding proteins or protein binding domains in the affinity purification of ligands, to mimic cc for the design of peptidomimetics, to replace intact binding proteins or protein binding domains in the affinity purification of ligands, to mimic cc epitopes in proteins to selectively raise polyclonal or monoclonal antibodies against such individual epitopes for isolating synthetic cc antibodies with a selected binding activity from plage display combinatorial libraries, to provide conformationally stable variants of peptides or proteins which exhibit floppy or unstable alpha-helical conformations of interest. This is the amino acid sequence of an HIV envelope protein gp41, fragments of which are used in the creation of constants.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 139; DB 6; Length 269; 100.0%; Pred. No. 9.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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/note= "hydrophobic region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
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(JACK-) JACKSON FOUND HENRY M.
(USSA ) US SEC OF ARMY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.v
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 269 AA;
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26-JUN-1998
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The present sequence represents HIV-1 gp160 residues 33-681 (the full protein is on the SWISS-PROT database Seq ID: 119434) used in a vaccine of the present invention. The vaccine composition is capable of eliciting contralising antibodies in a subject to a pathogenic organism which antibodies are present in vaginal secretions, intestinal secretions, lung secretions or facese. The vaccine comprisies: (a) an antigen comprising a protein or peptide having: (i) an endogenous hydrophobic material comprising a sequence of 3 to 50 non-polar or uncharged amino acids; (ii) added to the protein or peptide, an exogenous hydrophobic material comprising a sequence of 3 to 50 non-polar or uncharged amino acids or a 8-18C fatty acyl group, or (iii) both (i) and (ii), and (b) complexed with the antigen, a composition (complexed or coupled protein or peptide maintains a native structure of antigenic epitopes such that, upon administration to the subject, the antigen induces neutralising antibodies in one or more of vaginal continuations in manne response against a pathogenic organism such as a causative agent of a sexually-transmitted or mucosally-transmitted clieses, e.g. HIV infection. The compositions preserve the antigenic integrity of the protein or peptide epitopes while at the same time contains their immunogenicity. (Updated on 17-0CT-2003 to standardise OS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gpl20 protein; purification; fractionation; ion exchange; chromatography; binding affinity; CD4; hydrophobic interaction; size exclusion; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 649;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 139; DB 2; 100.0%; Pred. No. 2.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-1 gpl20 protein fragment from isolate CDC4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW43072 standard; peptide; 865 AA
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93US-00109002.
94US-00240073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100. Matches 29; Conservative
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11-SEP-1998 (first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 649 AA;
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AAW43066-W43080 are fragments of the gp120 protein from different human

Claim 9; Page 22; 62pp; English

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in a novel method for purifying HIV gpl20 so as to provide a purified gpl20 glycopeptide having protein/protein binding properties substantially identical to natural viral HIV gpl20. The method involves substantially identical to natural viral HIV gpl20. The method involves glycopylated gpl20 preparation containing full-length, glycopylated gpl20 using ion exchange chromatography so as to provide a first collection of fractions. A a fraction from the first collection is selected that exhibits specific binding affinity for CD4 peptide, thereby producing a first fractionated material. The first fractionated material is fractionated by hydrophobic interaction chromatography so as to provide a second collection of fractions from which a second collection is selected that exhibits specific binding affinity for CD4 peptide. This second fraction is fractionated by size exclusion chromatography so as to provide a third collection of fractions exhibiting specific binding affinity for CD4 peptide, thereby providing the purified gpl20 can be used for antibody production and in vaccines.

(Updated on 17-OCT-2003 to standardise OS field)
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immunodeficiency virus type I (HIV-1) isolates. These proteins are
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                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 139; DB 2; 100.0%; Pred. No. 3.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                               Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g112;
                                                                                          Gaps
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 are used in vaccines for prevention and treatment of HIV infection
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Pred. No. 2.9e-09;
1; Mismatches 1;
                                                          Score 131; DB 6;
Pred. No. 2.9e-09;
1; Mismatches 1;
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                                                          94.2%;
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93.1%;
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                                                                                        Conservative
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                                                    Query Match
Best Local Similarity
Matches 27; Conserv
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Best Local Similarity
Matches 27; Conserv
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                             Sequence 669 AA;
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                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glutamine.
                                                                                                                                                                                                                                                        ABP73117;
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                                                                                                                                                                                              RESULT 7
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genetic by

gp140, of

ABP73122

Synthetic

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The present sequence represents a truncated variant, designated gp140, of the Human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope glycoprotein mutant g14 (see ACC43021 and ABP73118). The specification describes mutated HIV-1 envelope glycoproteins that have at least two mutations at glycosylation sites, conserved among primary isolates, each consisting of replacement of AAC or AAT (for ABN) by CAG or CAA (for Gall). The mutated envelope glycoprotein polymucleotides and polypeptides are used in vaccines for prevention and treatment of HIV infection
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                                                                                                                                                                                                                                                                                 New mutated env gene of human immune deficiency virus, useful for vaccination, also derived polypeptides having asparagine replaced glutamine.
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Pred. No. 2.9e-09;
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                                                                                                                                                     Ataman-Oenal Y;
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                               06-SEP-2001; 2001FR-00011699.
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                                                                                                                                              Reynard F,
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N-PSDB; ACC43023.
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                                                                                   (INMR ) BIOMERIEUX
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                                                                                                                                              Bedin F,
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Matches
$2 \times \times
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a Human immunodeficiency virus type 1 (HIV-1) envelope glycoprotein mutant. The specification describes mutated HIV-1 envelope glycoproteins that have at least two mutations at glycosylation sites, conserved among primary isolates, each consisting of replacement of AAC or AAT (for A8n) by CAG or CAA (for Gln). The mutated envelope glycoprotein polymucleotides and polypeptides are used in vaccines for prevention and treatment of HIV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; gl4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 2.9e-09;
1; Mismatches 1; Indels
                                                                                                                                           Amino acid sequence of a HIV-1 envelope protein mutant.
                                                                                                                                                                                                          Envelope glycoprotein; HIV-1; vaccine; HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ataman-Oenal Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499 AVGWLGAMFLGFLGAAGSTWGAASLALTV 527
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                                                                                                                                                                                                                                                                                          Human immunodeficiency virus 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-2001; 2001FR-00011699
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93.1%;
                                                                                   (first entry)
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Human immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Loca 27; Conservē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-278759/27.
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glutamine.

ABP73120

RESULT 9 ABP73120

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Bedin F,

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Gaps

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genetic by

Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g14.

Human immunodeficiency virus 1.

Synthetic.

WO2003020755-A1

13-MAR-2003

06-SEP-2002; 2002WO-FR003039 06-SEP-2001; 2001FR-00011699

Amino acid sequence of HIV-1 envelope protein mutant g14

17-JUN-2003

ABP73118;

ABP73118 standard; protein; 844 AA.

RESULT 12

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by
             describes mutated HIV-1 envelope glycoproteins that have at least two mutations at glycosylation sites, conserved among primary isolates, each consisting of replacement of AAC or AAT (for Ann) by CAG or CAA (for Gln). The mutated envelope glycoprotein polymucleotides and polypeptides are used in vaccines for prevention and treatment of HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the Human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope glycoprotein mutent 912. The specification describes mutated HIV-1 envelope glycoproteins that have at least two mutations at glycosylation sites, conserved among primary isolates, each consisting of replacement of AAC or AAT (for ABN) by CAG or CAA (for Gln). The mutated envelope glycoprotein polynucleotides and polypeptides are used in vaccines for prevention and treatment of HIV infection
envelope glycoprotein mutant g112. The specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g12.
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mutated env gene of human immune deficiency virus, useful for vaccination, also derived polypeptides having asparagine replaced
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                                                                                                                                            94.2%; Score 131; DB 6; Length 844; 93.1%; Pred. No. 3.7e-09; ive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of HIV-1 envelope protein mutant g12
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                                                                                                                                                                                                               1 AVGMLGAMFLGFLGAAGSTMGATSMALTV
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                                                                                                                                                                                                                                                                                                                               ABP73112 standard; protein; 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
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                                                                                                                                                                              Conservative
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                                                                                                                          Query Match
Best Local Similarity
27; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bedin F, Reynard F,
(HIV-1) isolate 133
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                                                                                                              Sequence 844 AA;
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                                                                                                                                                                                                                                                                                               RESULT 11
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888888888
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New mutated env gene of human immune deficiency virus, useful for genetic vaccination, also derived polypeptides having asparagine replaced by

Claim 12; Page 102-103; 127pp; French.

glutamine.

Verrier B, Ataman-Oenal Y;

Reynard F,

Bedin F,

(INMR) BIOMERIEUX

WPI; 2003-278759/27.

N-PSDB; ACC43021

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 844;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Envelope glycoprotein; HIV-1; vaccine; HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.2%; Score 131; DB 6;
93.1%; Pred. No. 3.7e-09;
iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        499 AVGMLGAMFLGFLGAAGSTMGAASLALTV 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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es 27; Conservative
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Matches
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Gaps

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1 AVGMLGAMFLGFLGAAGSTMGATSMALTV

Local Similarity 93.1%; nes 27; Conservative

Best Loca Matches

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29

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Bedin F,

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The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HIV Env protein used in the scope of the invention.
The present sequence represents an envelope glycoprotein of Human describes mutated Virus type 1 (HIV-1) isolate 133. The specification describes mutated HIV-1 envelope glycoproteins that have at least two mutations at glycosylation sites, conserved among primary isolates, each consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for are used in vaccines for prevention and treatment of HIV infection. (Updated on 23-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a candidate peptide epitope, which induces a HLA class I CTL response comprises identifying variants of a peptide epitope 8-11 amino acids in length comprising primary anchor residues of the same HLA class
                                                                                                                                                                                                                                                              i, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sette A,
                                                                                                                                                                                                                         Score 131; DB 6;
Pred. No. 3.7e-09;
1; Mismatches 1;
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Pred. No. 4.7e-09;
                                                                                                                                                                                                                                                                                                                                               527
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                                                                                                                                                                                                                                                                                                                               AVGMLGAMFLGFLGAAGSTMGAASLALTV
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                                                                                                                                                                                                                         94.2%;
93.1%;
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93.1%;
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                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.1:
Matches 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immune stimulation; Env
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV Env protein #99.
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Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                   Sequence 844 AA;
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                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a Human immunodeficiency virus type 1 (HIV-1) envelope glycoprotein mutant. The specification describes mutated HIV-1 envelope glycoproteins that have at least two mutations at glycosylation sites, conserved among primary isolates, each consisting of replacement of AAC or AAT (for ABN) by CAG or CAA (for Gln). The mutated envelope glycoprotein polynucleotides and polypeptides are used in vaccines for prevention and treatment of HIV infection
                                                                                                                                                                                                                                           New mutated env gene of human immune deficiency virus, useful for genetic vaccination, also derived polypeptides having asparagine replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mutated env gene of human immune deficiency virus, useful for genetic vaccination, also derived polypeptides having asparagine replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene.
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                                                                                                                                         Ataman-Oenal Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.2%; Score 131; DB 6;
ilarity 93.1%; Pred. No. 3.7e-09;
Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 AVGMLGAMFLGFLGAAGSTMGAASLALTV 527
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                                                                                                                                                                                                                                                                                                                           Disclosure; Page 113-116; 127pp; French.
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                      06-SEP-2002; 2002WO-FR003039
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                                                          06-SEP-2001; 2001FR-00011699
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(first ent
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                                                                                               (INMR ) BIOMERIEUX SA
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Best Local Similarity
                                                                                                                                                                               2003-278759/27.
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N-PSDB; ACC43024.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 844 AA;
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RESULT 14

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Newman

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Gaps

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Length 791;

Search completed: March 7, 2006, 17:45:24 Job time : 12.7198 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

7, 2006, 17:45:48; Search time 2.22419 Seconds (without alignments) 1254.519 Million cell updates/sec

US-09-938-406-1_COPY_523_551 Title: Perfect score:

1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ω S	Description	env polyprotein -	env polyprotein pr		env protein - huma	envelope protein g	protein	protein	rotein p	tein	env protein - huma	1	envelope polyprote	env protein - huma	env protein - huma		envelope protein g		env polyprotein -	envelope polyprote	env polyprotein pr		env polyprotein pr			envelope polyprote	envelope protein g	env polyprotein M	envelope glycoprot	env protein - huma
SUMMARIES	. QI	VCLJH4	VCLJSC	860706	069098	S70417	822000	S22002	VCLJA2	VCLJ3W	860689	S60691	S60525	Se0693	S13288	T01672	S22004	S22006	833985	S54384	VCLJZR	VCLJH3	VCLJVL	S60696	860532	860531	S21994	A41621	T09448	S13289
	DB	<u>.</u> –	-	7	~	7	7	~	Н	Н	~	~	~	~	~	7	~	~	~	7		Н	-	'n	7	~	7	~	7	8
	Query Match Length	868	861	69	69	358	358	358	852	856	69	69	294	9	854	859	357	357	851	853	852	856	856	68	301	301	357	445	847	847
4	Query Match	100.0	91.4	89.2	88.5	87.8	87.8	87.8	86.3	9.58	83.5	82.0	81.7	80.2	. 79.5	79.5	78.8	78.8	78.8	78.8	78.8	78.8	78.8	78.1	78.1	78.1	78.1	78.1	78.1	78.1
	Score	139	127	124	123	122	122	122	120	119	116	114			110.5	110.5	109.5	109.5	•	109.5	109.5		109.5		108.5	108.5	108.5	108.5	•	108.5
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env polyprotein -	env polyprotein pr	envelope protein g	env protein - huma	env polyprotein pr	envelope protein g	envelope polyprote	env protein - huma	envelope polyprote	envelope polyprote						
VCLJBR	CLJLV	21998	S25940	H44001	S21990	S60545	S60524	S60541	360528	360543	860557	260556	S60707	860538	860521
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78.1	78.1 861 1	77.7 358 2	77.3 290 2		77.0	9.92	9.9/	9.92	76.6 299 2	76.6 299 2	76.6 300 2	9.92	75.9	75.9 297 2	75.9

ALIGNMENTS

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RESU	
2	:

env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)
NyAlternate names: coat polyprotein
NyAlternate names: coat polyprotein
NyContains: coat protein gpl20; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Accession: C25523
Reaguence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: C25523
Rajbanat, S.M.; Ralyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, EProc. Natl. Acad. Sci. U.S.A. 83, 880-884, 1986
A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human and parameter analysis of a distinct human and primary nucleotide sequence analysis of a distinct human and primary molecular changes.

A; Molecule type: DNA

A;Residues: 1-868 <DES> A;Cross-references: UNIPROT:P05879; UNIPARC:UPI000012A014; GB:M13137; NID:g326460; PIDN:

A;Gene: env

C;Superfamily: type E retrovirus env polyprotein C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protei F;1-521/Product: coat protein gp10 #status predicted <GP1> F;522-868/Product: coat protein gp41 #status predicted <GP2> F;89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459,

ö Query Match
100.0%; Score 139; DB 1; Length 868;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 29; Conservative 0; Mismatches 0; Indels

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Gaps

AVGMLGAMFLGFLGAAGSTMGATSMALTV 551 1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29

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env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)

N,Alternate names: coat polyprotein C,Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C,Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997

C;Accession: B28922
R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta Virology 164, 531-536, 1988
A;Title: Envelope sequences of two new United States HIV-1 isolates.
A;Reference number: A28922; MUID:88219542; PMID:3369091

A; Molecule type: DNA A; Residues: 1-861 <GUR>

A; Cross-references: UNIPARC: UPI0000174A39

C,Genetics:

C; Superfamily: type E retrovirus env polyprotein

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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                           env protein - human immunodeficiency virus type 1 (isolate 88) (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S60706
R;Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
A;Title: Molecular epidemiology of HIV-1 in Madrid.
A;Reference number: S60687; MUID:94249284; PMID:7545926
A;Accession: S60706
C;Kėywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote F;1-29/Domain: signal sequence #status predicted <SIG> F;30-861/Product: env polyprotein #status predicted <EPP> F;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396
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A/Status: preliminary; translation not shown
A/Nolecule type: DNA
A/Residues: 1-69 <ROJ>
A/Cross-references: UNIPROT:Q76153; UNIPARC:UPI0000101115; EMBL:Z29692; NID:g808981; PIC
C/Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q76161; UNIPARC:UP1000010624B; EMBL:Z2968B; NID:g808997; PIL
C;Superfamily: type E retrovirus env polyprotein
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870417
envelope protein gpl20/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment c;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: patient 3B
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            env protein - human immunodeficiency virus type 1 (isolate 2080) (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: 860690
E;Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
Virus Res, 31, 331-342, 1994
A;Title: Molecular epidemiology of HIV-1 in Madrid.
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                                                                                                                                   Length 861;
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                                                                                                                                                                                     2; Indels
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                                                                                                                                 Score 127; DB 1;
Pred. No. 7.1e-09;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 124; DB 2;
Pred. No. 1.5e-09;
3; Mismatches 1;
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86.2%; Pred. No. 2e-09;
                                                                                                                                                                                                                                                               516 AVGTIGAMFLGFLGAAGSTMGATSMTLTV 544
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                                                                                                                                 ch 91.4%; 1 Similarity 89.7%; 26; Conservative 1
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Best Local Similarity 86.2%;
Matches 25; Conservative
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Matches 25; Conservative
                                                                                                                                                      Local Similarity
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A; Residues: 1-69 <ROJ>
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virus type 1 in blood and cerebro
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A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determir A;Recerence number: $21990
A;Accession: $22000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: S22002
A,Molecule type: DNA
A)Readleus: 1-38 «STEL»
A)Restraction: 0.258 «STEL»
A)Cross-references: UNIPROT.Q78141; UNIPARC:UPI0000178609; EMBL:X61352; NID:g60186; PIDN:
R,Steuler, H, Storach-Haggenlocher, B.; Wildemann, B.
A,IDS Res. Hum. Retroviruses 8, 53-59, 1957, 1988
A,Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro A;Reference number: S70417; MUID:92144209; PMID:1736940
                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q78140; UNIPARC:UPI00000FB84C; EMBL:X61351; NID:g60184; PIDN:
C;Superfamily: type E retrovirus env polyprotein
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      envelope protein gpl20/gp41 - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate 3L
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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A;Cross-references: UNIPARC:UP10000104BB7; EMBL:X61352; NID:g60186
C;Superfamily: type B retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                              Length 358;
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                                                      A; Title: Distinct populations of human immunodeficiency A; Reference number: $70417; MUID:92144209; PMID:1736940 A; Recession: $70417 A; DID:92144209; PMID:1736940 A; Status: preliminary A; Catus: preliminary A; Residues: 1-358 <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 87.8%; Score 122; DB 2; Local Similarity 86.2%; Pred. No. 1.4e-08; es 25; Conservative 1; Mismatches 3
                                                                                                                                                                                                                                                                                                                              Score 122; DB 2;
Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
   B.; Wildemann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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R;Steuler, H.; Storch-Hagenlocher, B.; Will
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
                                                                                                                                                                                                                                                                                                                           87.8%;
ilarity 86.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                     25;
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Matches

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C, Accession: $60689
R;Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.; Vitus Res, 31, 311-342, 1994
A;Title: Molecular epidemiology of HIV-1 in Madrid.
A;Reference number: $60687; MUID: 94249284; PMID: 7545926
A;Accession: $60689
                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:Q76152; UNIPARC:UPI000010A870; EMBL:Z29691; NID:g808979; PID:
C,Superfamily: type E retrovirus env polyprotein
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A;Title: Molecular epidemiology of HIV-1 in Madrid.
A;Reference number: S60687; MUID:94249284; PMID:7545926
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C,Superfamily: type E retrovirus env polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           envelope polyprotein gp41 - human immunodeficiency virus type 1 (isolate CI-13-3 and iso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               С;Accession: S60525; S60527 —
R;Janssens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Fransen, K.; Motte, J.;
AIDS 8, 21-26, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q76169; UNIPROT:Q76170; UNIPARC:UPI0000102742; EMBL:X72028; A;Experimental source: isolate CI-13-3
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 env protein - human immunodeficiency virus type 1 (isolate D5/-2) (fragment)
C,Species: human immunodeficiency virus type 1, HIV-1
C,Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate CI-13-3; isolate CI-13-4
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                              env protein - human immunodeficiency virus type 1 (isolate 2051) (fragment)
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                                                                                                                                                         C,Species: human immunodeficiency virus type 1, HIV-1
C,Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change
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Pred. No. 1.7e-08;
3; Mismatches 3;
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Pred. No. 3e-08;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translation not shown A;Molecule type: DNA A;Residues: 1-69 <ROJ>
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Best Local Similarity 75.9%;
Matches 22; Conservative
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Best Local Similarity 79.37
Best Local Similarity 79.37
Conservative
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511
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N; Contains: coat protein gp120; coat protein gp41
C; Species: human immunodeficiency virus type 1, HIV-1
C; Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C; Accession: A24774
R; Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E. Cell 45, 637-648, 1986
A; Title: Identification and characterization of conserved and variable regions in the er A; Recenser number: A24774; MUD: 86218077; PMID: 2423250
A; Recension: A24774
A; Molecule type: DNA
A; Residues: 1.856 <STA>
A; Residues: 1.856 <STA>
A; Residues: 1.856 <STA>
A; Residues: env polyprotein; transmembrane protein
C; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: Betrovirus env polyprotein; transmembrane protein
C; Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
C; Keywords: coat protein gp120 #status predicted <GP1>F; 30-501/Product: coat protein gp41 #status predicted <GP2>F; 87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459
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82.8%; Pred. No. 7.8e-08;
iive 2; Mismatches 3; Indels.
                             Indels
86.2%; Pred. No. 1.4e-08;
                     1; Mismatches
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                                                                                                         13 AVGTIGAMFLGFLGAAGSTMGAASMTLTV 41
                                                                           1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
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                          Conservative
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Best Local Similarity
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nes 24; Conserv
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Best Local S
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Matches

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7, 2006, 17:51:35

Length 859; Indels

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Call 46, 63-74, 1966
A,Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolar, A, Accession: T0.672
A,Accession: T0.672
A,Accession:
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                                                                                                                                                C,Species: human immunodeficiency virus type 1, HIV-1
C,Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
                                                                                          envelope polyprotein precursor - human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 79.5%; Score 110.5; DB 2; Local Similarity 82.8%; Pred. No. 1e-06; les 24; Conservative 2; Mismatches 2;
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Job time : 3.22419 secs
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A;Accession: S60527
A;Status: nucleic acid sequence not shown; translation not shown
A;Folecule type: DNA
A;Aolecule type: DNA
A;Rosiques: 1-294 cJAW>
A;Cross-references: UNIPARC;UPI0000102742; EMBL:X72029; NID:g468633; PIDN:CRA50912.1; PJ
A;Experimental source: isolate CI-13-4
A;Experimental source: isolate CI-13-4
A;Experimental source: isolate CI-3-7
A;Conetics:
A;Conetics
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A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-68 <ROJ>
A;Cross-references: UNIPROT:Q76157; UNIPARC:UPI000010B1F0; EMBL:Z29684; NID:g808989; PIL
C;Superfamily: type E retrovirus env polyprotein
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A;Molecule type: DNA
A;Residues: 1-854 <OBR>
A;Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:O90178; UNIPROT:Q78243; UNIF
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C;Accession: S13288
R;O'Brien, W.A.; Koyanaqi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.R
Nature 348, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gpl20
A;Reference number: S13288; MUID:91043044; PMID:2172833
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Pred. No. 1.4e-07;
1; Mismatches 2; Indels 1.
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Pred. No. 1e-06;
2; Mismatches 2; Indels 1
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$13288
env protein - human immunodeficiency virus type 1
env protein - human immunodeficiency virus type 1, HIV-1
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Pred. No. 6.3e-08;
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Best Local Similarity 86.2%;
Matches 25; Conservative
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RESULT 15

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

on:

Run

7, 2006, 17:40:55; Search time 13.3024 Seconds (without alignments) 1538.097 Million cell updates/sec

US-09-938-406-1_COPY_523_551 ritle:

Perfect score:

1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	immun	immun	immun	immun	lmmun	Lmmun	tmmun	וששתח	וששתי	mmun	Lmmun	נחשמט	Lmmun	immun	Lmmun	Lmmun	Lmmun	וששחי	Lmmun	וששתם	mmun	immun	וששחם	-mmm	unum.	เทพมา	מתששו	immun	immun	immun
tion	human im	human im	human im	human im	human im	human im	human im	human im	human im	human i	human	human i	human	human	human im	human im	human	human	human	human	human i	human im								
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	ENV HV1C4	Q6IŪG0 9HIV1	UG1_9HIV1	Q6IUG2_9HIV1	Q6QLL1 9HIV1	Q6QLK5 9HIV1	561_9HIV1	Q6QLK7 9HIV1	LK8_9HIV1	Q6QLK9_9HIV1	LLO_9HIV1	Q6QLJ4 9HIV1	LJ5_9HIV1	LJ6_9HIV1	Q6QLJ7 9HIV1	Q6QLJ8_9HIV1	Q6QLJ9_9HIV1	LKO_9HIV1	Q6QLK1 9HIV1		Q6QLK3_9HIV1	Q6QLK4 9HIV1	Q6QLK6 9HIV1	Q6QLL3 9HIV1	Q7SUT2 9HIV1	P87924 9HIV1	27SUT4 9HIV1	Q7SUT6 9HIV1	Q7SUT7 9HIV1	C1SUT8 9HIV1
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Score	139	132	132	132	131	131	131	131	131	131	131	131	131	131	131	131	131	131	131	131	131	131	131	131	130	130	130	130	130	130
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130	129	128	128	128	128	128	128	128	128	128	127	127	127
32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN SEQUENCE OF 34-43.

MEDILINE-90253-224; PubMed=2187500;

MEDILINE-90253-224; PubMed=2187500;

Kalyanaraman V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,

DeVico A.L., Copeland T., Oroszlan S., Gallo R.C., Sarngadharan M.G.;

"Characterization of the secreted, native gp120 and gp160 of the human immunodeficiency virus type 1.";

AIDS Res. Hum. Retroviruses 6:371-380(1990).
                                                                                                                                                Human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1).
Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
                                  01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
                                                                                                                                                                                                                                                             MEDLINE=87041461; PubMed=3490666;
Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
Andersen P.R., Devare S.G.;
"Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences.";
Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384 (1986).
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Transmembrane glycoprotein.
N-linked (GlcNac. .) (Potential)
N-linked (GlcNac. ..) (Potential)
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PIR; C25523; VCLJH4.
HSSP; P19549; IMEQ.
SMR; P05879; 84-129, 87-212, 206-503, 552-638.
HIV; M13137; ENV$CD645.
InterPro; IPRO00328; Env GP41.
InterPro; IPRO0077; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
Pfam; PF00517; GP41; 1.
868 AA.
 STANDARD:
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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae, Lentivirus, Primate lentivirus group.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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SWR; QGIUGI; 80-134, 561-647.
                                                                                                                                                                       Length 877;
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Pred. No. 1.6e-08;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000228; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Envelope protein; Transmembrane.
SRQUENCE 877 AA; 99229 MW; D5F0E3B9A631EE3F CRC64;
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005199; F:structural molecule activity; IEA.
InterPro; IPR0000328; Env GP41.
InterPro; IPR0000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP120; 1.
AIDS; Bnvelope protein; Transmembrane.
SEQUENCE 877 AA; 99339 MW; 81FFF9C9641EB32C CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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QGIUG2_9HIV1 PRELIMINARY; PRT; 877 AA.
QGIUG2;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Lentivirus; Primate lentivirus group.
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Gorry P.R., Kunstman K.J., Morgan T., Moore J.P., Mascola J.R., Agoptan K., Holm G.H., Mehle A., Taylor J., Farzan M., Wang H., Ellery P., Willey S., Clapham P., Wolinsky S.M., Crowe S.M., Gabuzda D.;
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100.0%; Score 139; DB 1; Length 868;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 29; Conservative 0; Mismatches 0; Indels (
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QGIUGO;
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868 AA;
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ERBL; AKS53428; AAS58771.1; -; Genomic_RNA.
SMR; OGOLL1; 140-479, 528-614.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000375; P:regulation of transcription, DNA-dependent; IEA.
                          Gorry P.R., Kunstman K.J., Morgan T., Moore J.P., Mascola J.R., Agopian K., Holm G.H., Mehle A., Taylor J., Farzan M., Wang H., Ellery P., Willey S., Clapham P., Wolinsky S.M., Crowe S.M.,
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                                                                                                                                                                                                                                                                    Length 877;
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                                                                            Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AK624304; ART44417.1; -; Genomic_DNA.
HSSP; P04578; 1K33.
SWR; Q6IUG2; 80-134, 561-647..
                                                                                                                                                                                                                          AIDS; Envelope protein; Transmembrane.
SEQUENCE 877 AA; 99362 MW; 55212AEE17198A77 CRC64;
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                                                                                                                               GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:00019198; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
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Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus,
Primate lentivirus group.
                                                                                                                                                                                                                                                                 95.0%; Score 132; DB 2;
93.1%; Pred. No. 1.6e-08;
iive 1; Mismatches 1.
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93.1%; Pred. No. 2e-08;
ive 1; Mismatches 1.
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InterPro; IPR000777; GP120.
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QGQLL1;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                             Local Similarity 93.1 les 27; Conservative
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             NUCLEOTIDE SEQUENCE
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SEQUENCE 799 AJ
                                                                  Gabuzda D.;
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PubMed=15607649; DOI=10.1128/JVI.78.22.12625-12637.2004;
Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
Twolutionary Dynamics of the Glycan Shield of the Human
Immunodeficiency Virus Envelope during Natural Infection and
Implications for Exposure of the 2G12 Epitope.";
J. Virol. 78:12625-12637(2004).
I. J. Virol. 78:12625-12637(2004).
R EMBL, AY535434, AA558777.1; -; Genomic_RNA.
R MC) GO:00103131; C:viral envelope; IEA.
R GO: GO:00103131; C:viral envelope; IEA.
R GO: GO:00103131; C:viral envelope; IEA.
R GO: GO:0003700; F:transcription factor activity; IEA.
R GO: GO:0003700; F:transcription factor activity; IEA.
R GO: GO:0003285; Brucquial molecule activity; IEA.
R GO: GO:0003285; Rrucquial molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR000328; Env GP41.
InterPro; IPR000517; GP120.
R InterPro; PR000517; GP120.
R Pfam; PF000517; GP121.
R Pfam; PF000517; GP121.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99372987; PubMed=10445815; DOI=10.1089/088922299310548; Ataman-Onal Y., Coiffier C., Giraud A., Babic-Erceg A., Biron F.
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                                                Created)
Last sequence update)
Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus;
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AIDS Res. Hum. Retrovirues 15:1035-1039(1999).
EMBL; AF041126; AAC02517.1; -; Genomic_DNA.
HSSP; P04578; 1K34.
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     PRT;
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                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
QGQLKS 9HIV1 PRELIMINARY;
QGQLKS;
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Matches 27; Conservative
                                                                                                                                                                                                               Primate lentivirus group.
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01-JUN-1998 (TrEMBLrel.
                                                                                                                            Envelope glycoprotein.
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NUCLEOTIDE SEQUENCE.
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SEQUENCE 814 A
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Matches

1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29

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B., Barin F.;

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PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
"Evolutionary Dynamics of the Glycan Shield of the Human Immunodeficiency Virus Envelope during Natural Infection and Implications for Exposure of the 2G12 Epitope.";
J. Virol. 78:12625-12637(2004).
EMBL; AYS55430; AAS58773.1; -; Genomic_RNA.
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Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
        Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
                                                                                                                                                 Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., "Evolutionary Dynamics of the Glycan Shield of the Human Immunodeficiency Virus Envelope during Natural Infection and J. Wirol. 78:12625-12637 (2004).

EMBL, AX535431, AAS58774.1; -; Genomic_RNA.
                                                                                                                                PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
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SEQUENCE 844 AA; 95830 MW; DOFF96C9ACA018A8 CRC64;
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WCE 844 AA; 95761 MW; 5CEFA0F0FBE03C58 CRC64;
                                                                                                                                                                                                                                                                         SMR; Q6QLK8; 140-479; 528-614.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005198; R:ructural molecule activity; IEA.

InterPro; IRR000328; Env GP41.
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                         Lentivirus, Primate lentivirus group
NCBI_TaxID=11676;
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InterPro; IPR000777; GP120.
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QGQLK9;
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Pfam; PF00517; GP41; 1.
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Pfam; PF00517; GP41; 1.
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                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                             STRAIN=133;
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EMBL; AY535432; AA558775.1; -; Genomic_RNA. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:001528; F:structural molecule activity; IEA.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Pred. No. 2.1e-08;
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SMR; OS6561; 140-479, 528-614.

GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:001918; F:structural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
InterPro; IPR00077; GP120, 1.
Pfam; PF00517; GP120, 1.
Pfam; PF00517; GP41; 1.
AIDS; Envelope protein; Transmembrane.
SEQUENCE 844 AA; 95831 MW; CA255D577DE418A8 CRC64;
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QGQLK7;
QGJCJU-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last senotation update)
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SEQUENCE 844 AA; 95748 MW; 9C52681
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InterPro; IPR000777; GP120.
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                                                                                                                                                                                                                                                        93.1%;
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QGQLK8;
05-JUL-2004 (TEMBLrel. 27,
05-JUL-2004 (TEMBLrel. 27,
05-JUL-2004 (TEMBLrel. 27,
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"Evolutionary Dynamics of the Glycan Shield of the Human
Immunodefichency Virus Envelope during Natural Infection and
Implications for Exposure of the 2G12 Epitope.";
J. Virol. 78:12625-12637(2004)
R. EMBL; AY535429; AAS58772.1; -; Genomic_RNA.

SMR, OG0101010: C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016013; C:viral envelope; IEA.
R. Of GO:0016013; R:structural molecule activity; IEA.
R. InterPro; IPR00077; GP120.
R. Pfam; PF00514; GP120;
R. Pfam; PF00514; GP120;
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Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
Bvolutionary Dynamics of the Glycan Shield of the Human
Immunodeficiency Virus Envelope during Natural Infection and
Implications for Exposure of the 2G12 Epitope.";
J. Virol. 78:12625-12637(2004).
SMR; QG0LJ4; 200-494, 543-629.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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Lentivirus; Primate lentivirus group.
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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499 AVGMLGAMFLGFLGAAGSTMGAASLALTV 527
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QGQL34;
05-JJL-2004 (TEMBLFEl. 27,
05-JJL-2004 (TEMBLFEl. 27,
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QGQLLO;
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Best Local Similarity 93.1
Matches 27; Conservative
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Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
Imwanofeficiency Virus Envelope during Natural Infection and Implications for Exposure of the 2G12 Epitope.";
J. Virol. 78:12625-12637(2004).
EMBU; AYS35445; AAS58788.1; -; Genomic_RNA.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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                                                                                   AIDS; Envelope protein; Transmembrane.
SEQUENCE 859 AA; 97425 MW; 4845DE44A98C5EC7 CRC64;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR00028; EN GP41.
InterPro; IPR000777; GP120.
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Pred. No. 2.1e-08;
1; Mismatches 1;
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AIDS; Envelope protein; Transmembrane.
SEQUENCE 859 AA; 97398 MW; 8378D38
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1 Similarity 93.1%;
27; Conservative :
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QGQLJS;
                    Interpro, IPR000777; GP12
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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IPR000328;
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Best Local Similarity
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"Evolutionary Dynamics of the Glycan Shield of the Human
Immunodeficiency Virus Envelope during Natural Infection and
Immunodeficiency Virus Envelope during Natural Infection and
Immunodeficiency Virus Envelope during Natural Infection and
J. Virol. 78:12625-12637(2004).
J. Virol. 78:12625-12637(2004).
SMR: OGOLJ. 78:12625-12637(2004).
SMR: OGOLJ. 7:106-949, 543-629.
GO; GO:0016021; C:infegral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000777; GP120.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBL_TaxID=11676;
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Pred. No. 2.1e-08;
1; Mismatches 1; Indels
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Pred. No. 2.1e-08;
1; Mismatches 1; Indels
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PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
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AIDS; Envelope protein; Transmembrane.
SEQUENCE 859 AA; 97483 MW; 5B54B76D5F4245A8 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Envelope glycoprotein.
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Local Similarity 93.1%;
es 27; Conservative
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QGQLJ7;
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NUCLEOTIDE SEQUENCE
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Q6QLJ7_9HI
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Constrained Helical Peptides and Methods Making Same
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COMPUTER READABLE FORM:
MEDIUM TYPE: 35 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARRE: WinParin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TOrchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 36,700
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 139; DB 2;
100.0%; Pred. No. 2.8e-12;
iive 0; Mismatches 0;
                                     US-08-965-056-60
US-08-965-056-22
US-09-157-963-7
US-09-568-105-7
US-09-965-056-59
US-08-965-056-33
US-08-965-056-33
US-08-965-056-67
US-08-965-056-67
US-08-965-056-67
US-08-965-056-67
US-08-965-056-67
US-08-965-056-87
US-08-965-056-48
                                                                                                                                                                                                                                                                                       ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: J. Kevin Judice
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Hel:
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/08965056; Patent No. 6271198; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 29:
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LENGTH: 269 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            650/952-9881
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                             (without alignments)
789.495 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                               7, 2006, 17:51:03; Search time 3.03687 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/jaa/5_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6_COMB.pep:*
/cgn2_6/ptodata/1/jaa/H_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/jaa/RE_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-965-056-12
US-07-956-483-14
US-08-965-056-25
US-08-965-056-24
US-08-965-056-24
US-08-965-056-34
US-08-965-056-36
US-08-965-056-36
US-08-965-056-43
US-08-965-056-42
US-08-965-056-42
US-08-965-056-42
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US-08-965-056-42
US-08-965-056-42
US-08-965-056-42
US-08-965-056-42
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                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                       US-09-938-406-1_COPY_523_551
139
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Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
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Match Length
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Gaps

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Indels

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APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: Gristopher Phelan
APPLICANT: James A. Starovasnik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Constrained Helical Peptides and Methods of Making Same
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                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION TOWNER: US/08/965,056 FILING DATE: 05-No. 6271198-1997 CLASSIFATION: 530 ATTORNEY/AGENT INFORMATION: NAME: TOTChia, PhD., Timothy E. REGISTRATION NUMBER: 91005R2 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
APPLICANT: Robert S. McDowell
APPLICANT: Robert S. McDowell
APPLICANT: Melissa A. Starovasnik
APPLICANT: James A. Wells
                  Sequence 27, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 267 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 93.1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1 DNA Way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
US-08-965-056-27
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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US-08-965-056-47
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Sequence 12, Application US/08965056

Patent No. 6271198

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

APPLICANT: Andrew C. Braisted

APPLICANT: Andrew C. Braisted

APPLICANT: J. Kevin Judice

APPLICANT: J. Christopher Phelan

APPLICANT: Meliss A. Starovasnik

APPLICANT: Meliss A. Starovasnik

TITLE OF INVENTION: Constrained Helical Peptides and Methods of

TITLE OF INVENTION: Making Same

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STARE: California

CONDITY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.1%; Score 128; DB 2; Length 269; 89.7%; Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: 0C-DOS/MS-DOS SOFTWARE: Winheatin (Genentech) CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/965,056 FILING DATE: 05-No. 6271198-1997 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: Torchia, PhD., Timothy E. REGISTRATION NUMBER: 36,700 REPERENCE/DOCKET NUMBER: 91005R2 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: 650/25-8674 TELEFAX: 650/25-8674 TELEFAX: 650/95-9881 INFORMATION POR SEQ ID NO: 47: 550/BENERICE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94080
ZIP: 94080

CMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA: PDD. TIMOCHY E. REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 36,700
TELECOMMUTCATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFRAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 AVGVIGAMFLGFLGAAGSTMGAASMALTV 70
        South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.77
Matches 26; Conservative
                                  California
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42 AVGMLGAMFLGFLGAAGSTMGATSMALTV 70
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Sequence 5, Application US/08472240A
      US-08-472-240A-5
                                                  Patent No.
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                                                                                                                                                    Length 269;
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1 Similarity 89.7%; Pred. No. 5.5e-10;
26; Conservative 1; Mismatches 2; Indels
                                                                                                                                               Score 127; DB 2; Length 26 Pred. No. 1.5e-10; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOVEL HYBRID, SOLUBLE AND UNCLEAVED 92160 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,483
FILING DATE: 31-DEC-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AN
TITLE OF INVENTION: 9P160 VARIANT
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                            42 AVGTIGAMFLGFLGAAGSTMGATSMTLTV 70
                                                                                                                                                                                                                                       1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 017753-005
FELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 92/19742
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 05392
FILING DATE: 02-MAY-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-07-956-483-14
; Sequence 14, Application US/07956483
; Patent No. 6261799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: (703) 836-620
TELEPAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 855 amino acids
TYPE: amino acid
STRANDENNFOR
                                                                                                                                                  91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino Acid
                                                                                                                                                  Query Match
Best Local Similarity 89.7
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria
STATE: Virginia
                                                                                ; TOPOLOGY: Linear
US-08-965-056-12
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Best Local Similarity
Matches 26; Conserv?
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511 AVGTIGAMFLGFLGAAGSTMGATSMTLTV 539

RESULT 6

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Constrained Helical Peptides and Methods of Making Same
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                                                     SOLUBLE AND UNCLEAVED
                                                                                                                                                                                                         STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATION COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,240A
FILING DATE: 07-JUN-1995
CLASSIFICATION 435
PRIOR APPLICATION NUMBER: US 07/956,483
FILING APPLICATION NUMBER: 31-DEC-1992
ATTONENYAGENT INFORMATION:
GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBRID,
TITLE OF INVENTION: 99160 VARIANT
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 AVGTIGAMFLGFLGAAGSTMGATSMTLTV 570
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APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/08965056 Patent No. 6271198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Teskin, Robin L.
REGISTATION UNDHER: 35,030
REFERENCE/DOCKET NUMBER: 0177;
TELECOMMUNICATION INFORMATION:
TELEFONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS: not relevant
not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     887 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 James A. Wells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS LENGTH: 887 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: General DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-472-240A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-965-056-25
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Indels

Length 269;

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Query Match 90.6%; Score 126; DB 2; Best Local Similarity 89.7%; Pred. No. 2.1e-10; Matches 26; Conservative 1; Mismatches 2.
                                               LENGTH: 269 amino acids
TYPE: Amino Acid
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Matches 26; Conservative
           SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                  TYPE: Ami
TOPOLOGY:
                                                                                                                                                             US-08-965-056-32
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US-08-965-056-21
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APPLICANT: J. Kevin Judice
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: Melisse A. Starovasnik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 90.6%; Score 126; DB 2; Length 269; Best Local Similarity 89.7%; Pred. No. 2.1e-10; Matches 26; Conservative 2; Mismatches 1; Indels
                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible .
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION NUMBER: 35,700
ATTORNEY/ACENT INFORMATION:
NAME: TOrchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 10105R2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE G50/525-8674
TELEFRANCE G50/525-9874
TELEFRANCE CHARACTERISTICS:
**TONGRANTION FOR SEQ ID NO: 25:
**TO
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinParin (denentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-NO. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TOTCChia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 36,700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 32, Application US/08965056
; Patent No. 6271198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 269 amino acids
Amino Acid
California
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APPLICANT: Andrew
APPLICANT: J. Kevi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
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                                       COUNTRY:
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APPLICANT: J. Kevin Judice
APPLICANT: Sobert S. McDowell
APPLICANT: Robert S. McDowell
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: J. Christopher Phelan
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: J DNA Way
CITY: South San Francisco
STREET: Link Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.6%; Score 126; DB 2; Length 269; 89.7%; Pred. No. 2.1e-10; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MinPatin (Genentech)
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION NUMBER: 36,700
REGISTRATION NUMBER: 36,700
REFERENCE DOCKET NUMBER: 91005R2
TELEPHONE: 650/225-8674
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
42 AVGMLGAMFLGFLGAAGSTMGARSLTLTV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
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                                                                                                                                              Sequence 44, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:
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Patent No. 6271198
GENERAL INFORMATION:
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Constrained Helical Peptides and Methods of Making Same
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 79; 9.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 AVGTLGAMFLGFLGAAGSTMGAASVALTV 70
                                                                                                                                                                                                                                                                                                                                                                                                            89.2%; Score 124;
89.7%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSIEM:
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-NO. 6271198-1997
CLASSIFFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD. 7 Imothy E.
REGISTRATION NUMBER: 36,700
BPFREENCE/DOCKET NUMBER: P1005R2
                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA, PhD,, TIMOTHY E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELEPHONE: 650/22-8674
TELEPHONE: 650/22-9881
INFORMATION POR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: Amino Acid
                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-NO. 6271198-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: James A. Starovasnik
APPLICANT: James A. Wells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08965056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PIELECOMMUNICATION INFORMATION TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 269 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 89.7
Matches 26, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        650/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                  US-08-965-056-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-965-056-36
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                     APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Constrained Helical Peptides and Methods of TITLE OF INVENTION: Making Same NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 91005R2
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 125; DB 2;
Pred. No. 2.9e-10;
1; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 AVGALGALFLGFLGAAGSTMGAASMALTV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andrew C. Braisted
J. Kevin Judice
Schort S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 58, Application US/08965056 Patent No. 6271198 GENERAL INFORMATION:
Andrew C. Braisted
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                             STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 269 amino acids
Amino Acid
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Best Local Similarity 89.7
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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US-08-965-056-21
                                                                                                                                                                                                                                                                         STATE: Ca
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Gaps

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Constrained Helical Peptides and Methods of
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 AVGTLGAMFLGFLGAAGSTMGAASMTLTV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 124;
Pred. No. 4
                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: r.c.rosyrac.
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-NO. 6771198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 91005R2
TELECHONIS. 650/225-8674
TELEPHONE: 650/225-8814
TELEPHONE: 650/252-9881
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: J. Kevin Judice
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helititle OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/08965056
Patent No. 6271198
FITLE OF INVENTION: Making Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                           Genentech, Inc
                                                                                                STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.77
Best Local Similarity 26; Conservative
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
STREET: 1 DNA Way
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TOPOLOGY: Linear
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                                                                                                                                                                            COUNTRY: USA
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                              Gaps
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| Patent No. 6271198
| GENERAL INFORMATION:
| APPLICANT: Andrew C. Braisted
| APPLICANT: Andrew C. McDowell
| APPLICANT: Andrew A. Wellan APPLICANT: J. Christopher Phelan APPLICANT: J. Christopher Phelan APPLICANT: J. Christopher Phelan APPLICANT: James A. Wells
| APPLICANT: James A. Wells
| TITLE OF INVENTION: Constrained Helical Peptides and Methods of TITLE OF INVENTION: Making Same NUMBER OF SEQUENCES: 113
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: Cenentech, Inc. STREET: 1 DNA Way
| CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
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                         2; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
89.7%; Pred. No. 4e-10;
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                      1; Mismatches
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89.2%; Score 124; DE
Best Local Similarity
89.7%; Pred. No. 4e-1
Matches 26; Conservative 0; Mismatches
                                                                      1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
                                                                                                                    42 AVGTLGAMFLGFLGAAGSTMGAASVALTV 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: rc-bos,ros COERATING SYSTEM: rc-bos,ros CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: DATA
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phb., Timothy E. REGISTRATION NUMBER: 36,700
REPERENCE/DOCKET NUMBER: P1005R2
TELECHONIS. 650/225-8674
TELECHONIS. 650/225-8814
TELECHONE: 650/225-9814
TELECHONE: 650/225-9814
TELECHONE: GSO/225-9814
TELECHONE: GSO/225-9814
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TELECHONE: GSO/225-9814
TELECHONE: GSO/225-9814
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Patent No. 6271198
GENERAL INFORMATION:
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Amino Acid
                      26; Conservative
Best Local Similarity
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ZIP: 94080
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US-08-965-056-43
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US-08-965-056-46
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Search completed: March 7, 2006, 17:52:52 Job time : 4.03687 secs

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Query Match
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                                                                                      7, 2006, 17:51:52 ; Search time 9.4528 Seconds (without alignments) 1281.847 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-487-094-20

US-10-487-094-21

US-10-487-094-11

US-10-487-094-12

US-10-487-094-12

US-10-487-094-24

US-10-487-094-24

US-10-481-945-2

US-10-481-945-2

US-10-481-945-2

US-10-481-945-2

US-10-481-945-2

US-10-884-816-12

US-09-884-816-12

US-09-884-816-12

US-09-884-816-12

US-09-884-816-12

US-09-884-816-12

US-09-884-816-25

US-09-884-816-25
                                                                                                                                                                      1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
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                                                                                                                                                                                                                                         1867569 seqs, 417829326 residues
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                                                                                                                                              US-09-938-406-1_COPY_523_551
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Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Appl
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TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
                                                             Sequence
Seq
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Withbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-MAY-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: *UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: TOTCCHIA, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REGISTRATION NUMBER: 36,700
REGISTRATION INFORMATION:
TELEBRAK: 650/952-9881
INFORMATION FOR SEC ID NOS: 29:
                                                                                          US-09-854-816-6
US-09-854-816-23
US-09-854-816-24
US-09-854-816-54
US-09-854-816-54
US-10-844-658-1
US-09-854-816-38
US-09-854-816-38
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US-10-780-507-51
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US-09-854-816-34
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SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-854-816-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. WcDowell
J. Christopher Phelan
Melissa A. Starovasnik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/09854816; Patent No. US20020151473A1
GENERAL INFORMATION:
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Length 269;

Score 139; DB 3; Pred. No. 2.5e-10;

100.0%;

Gaps

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0; Indels

0; Mismatches

29; Conservative

Matches

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Sequence 17, Application US/10487094

Sequence 17, Application US/10487094

Publication No. US20050065320A1

GENERAL INFORMATION:
APPLICANT: REYNARD, Frederic
APPLICANT: REYNARD, Frederic
APPLICANT: ATAMAN-ONAL, Yasemin
TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THERE;
CURRENT APPLICATION NUMBER: US/10/487,094

CURRENT APPLICATION NUMBER: FR 01/11699

PRIOR APPLICATION NUMBER: FR 01/11699

PRIOR APPLICATION NUMBER: PR 01/11699

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 17

LENGTH: 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NESOUR SEQUENCE 20, Application US/10487094

Sequence 20, Application US/10487094

Sequence 20, Application US/10487094

Sequence 20, Application US/10487091

Sequence 20, Application US/10487081

Sequence 20, Application US/10487081

APPLICANT: BENENARD. Frederic

APPLICANT: RERYBARD. Frederic

APPLICANT: WERNIER, Bernard

APPLICANT: WINTION: MUMBER: US/10/487,094

CURRENT APPLICATION NUMBER: US/10/487,094

CURRENT APPLICATION NUMBER: FR 01/11699

PRIOR FILING DATE: 2001-09-06

SEQ ID NO 20

LENGTH: 669

TYPE: PRT

CREANIER: FRT

CREANIER: HIV-1 mutant 914

US-10-487-094-20
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Pred. No. 7.4e-09;
1; Mismatches 1; Indels
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Best Local Similarity 93.1%; Pred. No. 7.4e-09;
Matches 27; Conservative 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: HIV-1 mutant g112
US-10-487-094-17
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US-10-487-094-14

i Sequence 14, Application US/10487094

i Publication No. US20050065320A1

i GENERAL INFORMATION:

APPLICANT: BEDIN, Frederic

APPLICANT: WERNER, Bernard

APPLICANT: ATAMAN-ONAL, Yasemin

TITLE OF INVENTION: MOTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THER

FILE REFERENCE: 118745

CURRENT APPLICATION NUMBER: US/10/487,094

CURRENT FILING DATE: 2004-02-19

PRIOR PAPLICATION NUMBER: FR 01/11699

PRIOR PELING DATE: 2001-09-06

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.1

LENGTH: 669
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Pred. No. 7.4e-09;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: LOWell, George
APPLICANT: LOWell, George
APPLICANT: Deborah
TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES FOR
TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES FOR
TITLE OF INVENTION: NUMBER: US/09/938,406
CURRENT APPLICATION NUMBER: US/09/938,406
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/214,701
PRIOR APPLICATION NUMBER: PCT/US 97/12253
PRIOR PILING DATE: 1999-09-30
PRIOR FILING DATE: 1997-07-10
PRIOR PILING DATE: 1997-07-10
PRIOR PILING DATE: 1997-07-10
SPRIOR FILING DATE: 1996-07-10
SPRIOR FILING DATE: 1997-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 8.6e-10;
Matches 29; Conservative 0; Mismatches 0;
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1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
                                                   42 AVGMLGAMFLGFLGAAGSTMGATSMALTV 70
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; Patent No. US20020155120A1
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ORGANISM: HIV-1 mutant g12
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ORGANISM: Virus HIV-1
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nes 27; Conserva
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Best Local S:
Matches 27,
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Sequence 15, Application US/10487094

Sequence 15, Application US/10487094

Publication No. US20050065320A1

GENERAL INFORMATION:

APPLICANT: BEDIN, Frederic

APPLICANT: REFERENCE

APPLICANT: ATAMAN-ONAL, Yasemin

TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THER

FILE REFERENCE: 118745

CURRENT APPLICATION NUMBER: US/10/487,094

CURRENT APPLICATION NUMBER: FR 01/11699

PRIOR FILING DATE: 2004-02-19

PRIOR APPLICATION NUMBER: FR 01/11699

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.1

SOFTWARE: Patentin Ver. 2.1

TYPE: PRIOR
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APPLICANT: RESTRAND, Prederic
APPLICANT: VERRIER, Bernard
APPLICANT: ATAMAN-ONAL, Yasemin
TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THER
FILE REPERENCE: 118745
CURRENT APPLICATION NUMBER: US/10/487,094
CURRENT FILING DATE: 2004-02-19
PRIOR PPLICATION NUMBER: FR 01/11699
PRIOR PILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                Length 844;
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Pred. No. 9.5e-09;
1; Mismatches 1;
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Pred. No. 9.5e-09;
1; Mismatches 1.
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Publication No. US20050065320A1
GENERAL INFORMATION:
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Best Local Similarity 93.1%;
Matches 27; Conservative
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Best Local Similarity 93.1%;
Matches 27; Conservative
; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 12; LENGTH: 844; TYPE: PRT; TYPE: PRT; ORGANISM: HIV-1 mutant g12 US-10-487-094-12
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US-10-487-094-15
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SEQ ID NO 18
LENGTH: 844
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ORGANISM: HIV-1 mutant g14
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Best Local Similarity
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APPLICANT: WERNIER, Bernard
APPLICANT: ATAMAN-ONAL, Yasemin
TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THER
FILE REFERENCE: 118745
CURRENT APPLICATION NUMBER: US/10/487,094
CURRENT PILING DATE: 2004-02-19
PRIOR PILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 11
LENGTH: 844
APPLICANT: VERRIER, Bernard
APPLICANT: ATAMAN-ONAL, Yasemin
TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THER
FILE REFERENCE: 118745
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APPLICANT: REYNARD, Frederic
APPLICANT: VERRIER, Bernard
APPLICANT: VARANEN, Bernard
APPLICANT: ATAMAN-ONAL, Yasemin
TITLE OP INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THER
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Pred. No. 7.4e-09;
1; Mismatches 1;
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                                                                                    CURRENT APPLICATION NUMBER: US/10/487,094
CURRENT FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: FR 01/11699
PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 669
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CURRENT FILING DATE: 2004-02-19
FRICH APPLICATION NUMBER: FR 01/11699
PRIOR PLILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 26
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Publication No. US20050065320A1
GENERAL INFORMATION:
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Publication No. US20050065320A1
GENERAL INFORMATION:
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Best Local Similarity 93.1%;
Matches 27; Conservative
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US-10-487-094-25
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ORGANISM: HIV-1 133
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Gaps

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1; Indels

1; Mismatches

27; Conservative

Matches

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APPLICANT: MULLINS, James I.
APPLICANT: RODRIGO, Allen G.
APPLICANT: LEARN, Gerald H.
APPLICANT: L. Fusheng
APPLICANT: NCKLE, David C.
APPLICANT: JENSEN, Mark A.
ITITE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOSEILE REFERENCE: 16336-001320US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                             APPLICANT: ROSIGO, Allen
APPLICANT: ROSIGO, Allen
APPLICANT: ROSIGO, Howard A.
APPLICANT: ROSIGO, Howard A.
APPLICANT: MILIANG, James I.
TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
FILE REFERENCE: 08987-012001
CURRENT APPLICATION NUMBER: US/10/441,949
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: PCT/US01/05288
PRIOR APPLICATION NUMBER: Q 60/183,659
PRIOR PLILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 66
SOTTOWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 2: SEQ ID NOS: 66
LENGTH: 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.5%; Score 130; DB 4; L
Best Local Similarity 93.1%; Pred. No. 1.4e-08;
Matches 27; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Artificially generated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 130; DB 5;
Pred. No. 1.4e-08;
0; Mismatches 2
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PRIOR APPLICATION NUMBER: US 10/204,204
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 883
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CURRENT FILING DATE: 2004-02-17
                              Sequence 2, Application US/10441949
Publication No. US20040116684A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10780507
Publication No. US20050137387A1
GENERAL INFORMATION:
APPLICANT: MULLINS, James I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 93.1%;
Matches 27; Conservative
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APPLICANT: BENNARD, Frederic
APPLICANT: REYNARD, Frederic
APPLICANT: ATAMAN-ONAL, Yasemin
APPLICANT: ATAMAN-ONAL, Yasemin
FILLE REFERENCE: 118745
CURRENT APPLICATION NUMBER: US/10/487,094
CURRENT APPLICATION NUMBER: FR 01/11699
PRIOR APPLICATION NUMBER: FR 01/11699
PRIOR APPLICATION NUMBER: FR 01/11699
ROOF REGION OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 844
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larity 93.1%; Pred. No. 9.5e-09;
Conservative 1; Mismatches 1; Indels
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93.1%; Pred. No. 1.4e-08;
cive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10441926
| Publication No. US20040115621A1
| GENERAL INNORMATION:
| APPLICANT: Rodrigo, Allen
| APPLICANT: Rodrigo, Allen
| APPLICANT: Rodrigo, Allen
| APPLICANT: Mullins, James I.
| TILLE REFERENCE: 08987-011001
| CURRENT APPLICATION NUMBER: US/10/441,926
| FILE REPERENCE: 08987-011001
| CURRENT PILING DATE: 2003-05-19
| PRIOR FILING DATE: 2001-02-18
| PRIOR FILING DATE: 2000-02-18
| NUMBER OF SEQ ID NOS: 42
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Artificially generated peptide US-10-441-926-2
                                             499 AVGMLGAMFLGFLGAAGSTMGAASLALTV 527
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1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
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Publication No. US20050065320A1
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ORGANISM: Artificial Sequence
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ORGANISM: HIV-1 mutant g22
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Best Local Similarity
Matches 27; Conserv
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LENGTH: 883
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PPLICANT: MULLINS, James I.
PPLICANT: RODRIGO, Allen G.
PPLICANT: LEARN, Gerald H.
PPLICANT: LIARN, Gerald H.
PPLICANT: LI, Fueheng
PPLICANT: NICKLE, David C.
PPLICANT: 1805EN, MARK A.
PPLICANT: 1803-001320US
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93.5%; Score 130; DB 5; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08;
Matches 27; Conservative 0; Mismatches 2; Indels
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US-10-780-507-121
                                  538 AVGMLGAMFLGFLGAAGSTMGAASMTLIV 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 103-7013-205
CURRENT FILING DATE: 2004-02-17
PRIOR APPLICATION NUMBER: US 10/204,204
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: PCT/US01/05288
PRIOR PILING DATE: 2000-02-18
PRIOR PILING DATE: 2000-02-18
PRIOR PILING DATE: 2000-02-18
PRIOR FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PATENT NOS: 125
LENGTH: 883
1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
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Publication No. US20050137387A1
GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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Search completed: March 7, 2006, 17:56:39 Job time : 10.4528 secs

1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29

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Sequence 13, Application US/11042988

Sequence 13, Application US/11042988

Publication No. US20050244818A1

GENERAL INFORMATION:

APPLICANT: SILICIANO, ROBERT

APPLICANT: ZHOU, YANII

APPLICANT: ZHOU, YANII

TITLE OF INVENTION: DUGG RESISTANCE

TITLE OF INVENTION: DUGG RESISTANCE

FILE REFERENCE: 62760(71699)

CURRENT APPLICATION NUMBER: US/11/042,988
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US-10-510-947-8
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l Similarity 82.8%;
24; Conservative
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Best Local Similarity
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TYPE: PRT
                                          Matches
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7, Appli
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12977, A
                                                                                                                           7, 2006, 17:53:05; Search time 1.11209 Seconds (without alignments) 521.549 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US11 NEW PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-141-725-14
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US-11-1014-842A-33

US-11-014-842A-33

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US-11-014-842A-39

US-11-022-562-219

US-11-014-842A-31

US-11-014-842A-31

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US-11-014-842A-31

US-11-07-092A-11

US-11-07-092A-11

US-11-067-092A-11

US-11-067-092A-11

US-11-067-092A-11

US-11-016-542-5

US-11-223-69A-7
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                                                                                                                                                                                                                                                                                                                                                                 135346 seqs, 20000420 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match 1
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Gaps

1;

Indele

Length 856;

Score 109.5; DB 6; Pred. No. 5.2e-07;

2; Mismatches

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Sequence 28, Appl
Sequence 12877, A
Sequence 12843, A
Sequence 12986, A
Sequence 12986, A
Sequence 127, App
Sequence 176, App
Sequence 176, App
Sequence 950, App
Sequence 950, App
Sequence 951, App
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                                               US-11-022-562-340

US-11-045-024-12943

US-11-045-024-12869

US-11-022-562-217

US-11-022-562-176

US-11-022-562-176

US-11-045-024-948

US-11-045-024-950

US-11-045-024-951

US-11-045-024-951

US-11-045-024-967

US-11-045-024-977

US-11-045-024-977

US-11-045-024-917

US-11-045-024-917

US-11-045-024-917

US-11-045-024-917

US-11-045-024-917

US-11-045-024-917
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ORGANISM: Human immunodeficiency virus type
                     US-11-014-842A-37
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| Sequence 37, Application US/2060013826A1
| Publication No. US2060013826A1
| GENERAL INFORMATION:
| APPLICANT: TANGY, FREDERIC
| APPLICANT: DELEBECQUE, FREDERIC
| APPLICANT: DELEBECQUE, FREDERIC
| TITLE OF INVENTION: ANTIGENS OF TITLE OF INVENTION: VACCINE COMPOSITIONS
| FILE REFERENCE: 2356.0093
| CURRENT APPLICATION NUMBER: US/11/014,842A
| FILE REFERENCE: 2356.0093
| CURRENT FILING DATE: 2003-06-20
| PRIOR FILING DATE: 2003-06-20
| PRIOR FILING DATE: 2003-06-20
| PRIOR FILING DATE: 2003-06-20
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE: PATCHIN VOE: 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/11135235
Publication No. US20060019395A1
GENERAL INFORMATION:
HAPLICANT: Marasco, Wayne
TITLE OF INVENTION: Lentiviral Vectors and Uses Thereof
FILE REFERENCE: 20363-027
CURRENT APPLICATION NUMBER: US/11/135,235
CURRENT FILING DATE: 2005-05-23
PRIOR PILING DATE: 2004-07-21
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Version 3.2
LENGTH: 856
                                                                                                                                                           TYPE: PRT (ACREANISM: Human immunodeficiency virus type 1 US-11-042-988-13
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ORGANISM: Human immunodeficiency virus type 1
US-11-135-235-1
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CURRENT FILING DATE: 2005-01-25
PRIOR APPLICATION UNDBER: 60/540,716
PRIOR FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 3.3
LENGTH: 856
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Best Local Similarity 82.8%;
Matches 24; Conservative 2
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Best Local Similarity 82.8
Matches 24; Conservative
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US-11-014-842A-37
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SEQ ID NO 37
LENGTH: 601
TYPE: PRT
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US-11-135-235-1
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US-11-014-842A-29

Sequence 29, Application US/11014842A

Sequence 29, Application US/11014842A

Publication No. US20060013826A1

GENERAL INFORMATION:
APPLICANT: TANGY, REEDERIC

APPLICANT: DOLLET, LUCILE

APPLICANT: DELEBECQUE, FREDERIC

TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF

TITLE OF INVENTION: VACCINE COMPOSITIONS

FILE REFRERENCE: 236.0093

CURRENT FILING DATE: 2004-12-20

FRIOR PELLING DATE: 2003-06-20

PRIOR FILING DATE: 2003-06-20

PRIOR FILING DATE: 2002-06-20

PRIOR FILING DATE: 2002-06-20

WUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 3.3

LENGTH: 669

TABLE OF 
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APPLICANT: LORIN CLARISSE
APPLICANT: LORIN CLARISSE
APPLICANT: HOLLET, LUCILE
APPLICANT: MOLLET, LUCILE
APPLICANT: MOLLET, LUCILE
TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
TITLE OF INVENTION: VACCINE COMPOSITIONS
FILE REFERENCE: 2356.0093
CURRENT APPLICATION NUMBER: PCT/EP03/07146
FRIOR APPLICATION NUMBER: PCT/EP03/07146
FRIOR APPLICATION NUMBER: PCT/EP03/07146
FRIOR APPLICATION NUMBER: PCT/EP03/07146
FRIOR PILING DATE: 2002-06-20
FRIOR PILING DATE: 2002-06-20
FRIOR PILING DATE: 2002-06-20
FRIOR PILING DATE: 2002-06-30
SOFTWARE: PARENTING DATE: 2002-06-30
SOFTWARE: PARENTING DATE: 2002-06-30
FRIOR FILING DATE: 2002-06-30
FRIOR PILING DATE: 2003-06-30
FRIOR PILING DATE: 2003-06-30
FRIOR FILING DATE: 2004-06-30
FRIOR FILING DATE: 2004-06-30
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FRIOR FILING DATE: 2007-06-30
FRIOR FILING DATE: 2007-06-3
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             Length 601;
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Score 104.5; DB 7;
Pred. No. 1.6e-06;
3; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human immunodeficiency virus type 1
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Publication No. US20060013826A1
GENERAL INFORMATION:
Query Match 75.2%;
Best Local Similarity 79.3%;
Matches 23; Conservative
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US-11-022-562-219
; Sequence 219, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
    APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
                                                                                                                                                                                                                                                                           Sequence 35, Application US/11014842A Publication No. US20060013826A1
                       75.2%;
                       Query Match
Best Local Similarity 79.33
Matches 23; Conservative
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Best Local Similarity 79.3
Matches 23; Conservative
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LENGTH: 801
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LENGTH: 854
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Publication No. US20060013826A1
GENERAL INFORMATION:
APPLICANT: TANGY, FREDERIC
APPLICANT: LOCILE
APPLICANT: LOCILE
APPLICANT: NOLLET, LUCILE
APPLICANT: NUMERINO: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
TITLE OF INVENTION: VACCINE COMPOSITIONS
FILE REFERENCE: 2356.0093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 39, Application US/11014842A
Publication No. US20060013826A1
GENERAL INFORMATION:
APPLICANT: TANGY, FREDERIC
APPLICANT: LORIN, CLARISSE
APPLICANT: DELEBECQUE, FREDERIC
TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
TITLE OF INVENTION: VACCINE COMPOSITIONS
TITLE OF INVENTION: VACCINE COMPOSITIONS
                                      Score 104.5; DB 7; Length 669;
Pred. No. 1.8e-06;
3; Mismatches 2; Indels 1:
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Pred. No. 1.8e-06;
3; Mismatches 2; Indels 1.
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; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-39
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; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-25
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CURRENT FILING DATE: 2004-12-20
FRIOR APPLICATION NUMBER: CT/EPD3/07146
FRIOR FILING DATE: 2003-66-20
FRIOR FILING DATE: 2003-66-20
FRIOR FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TILE REFERENCE: 2356.0093
CURRENT APPLICATION NUMBER: US/11/014,842A
CURRENT PILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: PCT/EP03/07146
PRIOR PILING DATE: 2003-06-20
PRIOR PILING DATE: 2002-06-20
PRIOR PILING DATE: 2002-06-20
PRIOR PILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET. 3.3
                                                                                                                                                             498 AVG-IGAVFLGFLGAAGSTMGAASVTLTV 525
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                                             75.2%;
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                                   Query Match
Best Local Similarity 79.3
Matches 23; Conservative
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Best Local Similarity 79.3
Matches 23; Conservative
US-11-014-842A-29
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LENGTH: 789
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GENERAL INFORMATION:
APPLICANT: LORIN, CLARISSE
APPLICANT: LORIN, CLARISSE
APPLICANT: MILET, LUCTILE
APPLICANT: MILET, LUCTILE
APPLICANT: MILET, LUCTILE
APPLICANT: MILET, LUCTILE
APPLICANT: DELEBECQUE, FREDERIC
TITLE OF INVENTION: AATIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
TITLE OF INVENTION: AATIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
TITLE OF INVENTION: AATIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
TITLE OF INVENTION: AATIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
TITLE OF INVENTION: AATIGENS OF SOON OF
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REPRENCE: DFN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT APPLICATION NUMBER: PCT/US03/20322
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR PILING DATE: 2003-06-27
PRIOR PILING DATE: 2003-06-27
PRIOR PILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FRASESQ for Windows Version 4.0
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     Length 789;
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     DB 7;
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79.3%; Pred. No. 2.4e-06;
tive 3; Mismatches 2;
Score 104.5; DB 7
Pred. No. 2.2e-06;
3; Mismatches 2;
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ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 AVG-IGAVFLGFLGAAGSTMGAASVTLTV 469
                                                                                                                                                                                                                                                                             430 AVG-IGAVFLGFLGAAGSTMGAASVTLTV 457
                                                                                                                                                                                                                  1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
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US-11-096-725-35
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                                                                                                                                                                   Sequence 31, Application US/11014842A

Sequence 31, Application US/11014842A

Bublication No. US20060013826A1

GENERAL INFORMATION:

APPLICANT: TANGY, FREDERIC

APPLICANT: TORIN, CLARISSE

APPLICANT: DELEBECQUE, FREDERIC

TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF

TITLE OF INVENTION: ANTICENS OF MAY VIRUSES - USE FOR THE PREPARATION OF

TITLE OF INVENTION: VACCINE COMPOSITIONS

FILE REFERENCE: 2356.0093

CURRENT APPLICATION NUMBER: US/11/014,842A

CURRENT APPLICATION NUMBER: PEP 02291550.8

PRIOR PILING DATE: 2003-66-20

PRIOR FILING DATE: 2002-66-20

PRIOR FILING DATE: 2002-66-20

PRIOR FILING DATE: 2002-66-20

PRIOR FILING DATE: 2002-66-20

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 3.3

LENGTH: 857
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APPLICANT: TANGY, CLARISSE
APPLICANT: LORIN, CLARISSE
APPLICANT: LORIN, CLARISSE
APPLICANT: MOLLET, LUCILE
TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF TITLE OF INVENTION: VACCINE COMPOSITIONS
FILE REFERENCE: 2356.0093
CURRENT PILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: PCT/FP03/07146
PRIOR FILING DATE: 2003-06-20
PRIOR FILING DATE: 2003-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
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; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-27
                             510 AVG-IGAVFLGFLGAAGSTMGAASITLTV 537
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  1 AVGMLGAMFLGFLGAAGSTMGATSMALTV 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 27
LENGTH: 869
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APPLICANT: CHEN, LISHAN
APPLICANT: CUI, KOUNTUAN
APPLICANT: CUI, KOUNTUAN
APPLICANT: CUI, KOUNTUAN
APPLICANT: MAYER, SASHA
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR DELIVERY OF
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: PHARMACEUTICAL
FILE REFERENCE: 04-03CTP
CURRENT APPLICATION NUMBER: US/1/223,699A
CURRENT APPLICATION NUMBER: 11/121,566
PRIOR FILING DATE: 2005-09-04
PRIOR APPLICATION NUMBER: 60/65,72
PRIOR APPLICATION NUMBER: 60/65,572
PRIOR APPLICATION NUMBER: 60/613,416
PRIOR APPLICATION NUMBER: 60/50,513
PRIOR PILING DATE: 2004-09-27
PRIOR PILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/570,513
PRIOR PILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/50,512
PRIOR PILING DATE: 2004-05-12
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                                                                                                                                                                                                                                        JUNEAURO 32-35
Sequence 35, Application US/11096725
Publication No. US20060013820A1
SEGRERAL INFORMATION:
APPLICANT: BONNATION:
APPLICANT: BROWN, Carlton B
SAPPLICANT: GEORGES, Bertrand
APPLICANT: STER, Philip U
TITLE OF INVENTION: Annigen Delivery Vectors and Constructs
FILE REFERENCE: KLB-001
FILE REFERENCE: Annigen Delivery Vectors and Constructs
FILE REFERENCE: KLB-001
FILE REFERENCE: KLB-001
FILE REFERENCE: KLB-001
STEROR APPLICATION NUMBER: GB0408164.2
FRIOR PILING DATE: 2004-04-01
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 40
SOFTWARE: Patentin version 3.2
LENGTH: 35
TYPE: PRT
CORGANISM: Human immunodeficiency virus type 1
US-11-096-725-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 71.6%; Score 99.5; DB 7; Best Local Similarity 88.0%; Pred. No. 3.1e-07; Matches 22; Conservative 1; Mismatches 1;
510 AVG-IGAVFLGFLGAAGSTMGAASVTLTV 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AVGMLGAMFLGFLGAAGSTMGATSM 25
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Publication No. US20060035815A1
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CHEN, YUCHING
APPLICANT: MAYER, SASHA
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DELIVERY OF
TITLE OF INVENTION: NUCLEIC ACIDS INTO CELLS AND FOR MODIFYING EXPRESSION
TITLE OF INVENTION: OF TARGET GENES IN CELLS
FILE REPRESENCE: 04-03US
CURRENT APPLICATION NUMBER: US/11/121,566A
                                                                                                                     Gaps
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: peptide US-11-223-699A-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-11-121-566A-96
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                                                                        Score 84; DB 7; Length 28;
Pred. No. 2.6e-05;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-11-121-566A-96
Sequence 96, Application US/11121566A
Publication No. US20060040882A1
GENERAL INFORMATION:
APPLICANT: CHEN, LISHAN
APPLICANT: CUI, KUNYUAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/568,027
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 163
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 96
LENGTH: 28
                                                                                                                                                                            1 GALFLGFLGAAGSTMGAWS 19
                                                                                                                                                      6 GAMFLGFLGAAGSTMGATS 24
                                                                          Query Match 60.4%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 89.5
Matches 17; Conservative
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Mismatches

Search completed: March 7, 2006, 17:57:11 Job time : 2.11209 secs

1 GALFLGFLGAAGSTMGAWS 19

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6 GAMFLGFLGAAGSTMGATS 24

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7, 2006, 17:40:32 ; Search time 262.28 Seconds (without alignments) 1087.222 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                   protein search, using sw model
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1 ANLWVTVYYGVPVWKEATTT......QNQQEKNQQELLQLDKWASL 649 US-09-938-406-1_COPY_33_681 **BLOSUM62** Scoring table: Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5

2443163 segs, 439378781 residues Searched:

2443163

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2005s:* A Geneseq 21:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

.* Query Result

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tior			_		~					_					4 HI	7 H	5 An				•			
Description	Aaw44250	Aaw43072	Aeb10584	Aab82761	Adw3834	Ady27998	Aeb10654	Aeb10552	Adz07749	Aeb10583	Ady99903	992	992	775	1779	Adz07797	Abr55495	Abr55684	Adc13218	Adw48030	Aay97073	Ado05103	Adz82338	Abu66565
Desc	Aawa	Aaw4	Aeb1	Aabe	Adw3	Ady2	Aeb1	Aeb1	Adzo	Aeb1	Ady9	Adys	Ady9	Adzo	Adzo	Adzo	Abr5	Abrs	Adcı	Adw4	Aay9	Ado	Adz8	Abu6
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	AAW44250	4AW4307	AEB10584	AAB8276	ADW3834	ADY27998	AEB1065	AEB1055	ADZ07749	AEB10583	ADY9990.	ADY9992	ADY99929	ADZ0775	ADZ07794	797797	ABR55495	ABR55684	ADC13218	ADW4803(4AY9707	AD005103	4DZ82338	ABU66565
Ħ	AAW	AAW	AEB	AAB	Ä	ADY	AEB	AEB	ADZ	AEB	ADY	ADY	Š	ADZ	ADZ	ADZ	ABR	ABR	ă	ADW.	Æ	ğ	ADZ	ABU
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Match Length DB	49	865	62	83	83	183	183	83	20	862	42	89	2602	41	41	40	99	842	42	42	47	47	847	842
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Score	3457	3388	2987	2977	2977	2977	2977.5	977	29	5	5	2947	2947	2939.5	2927.5	2922	2891	2883	2883	2883	2883	2883	883	878
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Adm73868 HIV-1 pol	Abb06211 HIV Env i	Adx39692 HIV Env p	Adz04164 Env prote		Adk14406 HIV wild-		Adk14404 HIV mutan	Adx39677 HIV Env p	Adx39681 HIV Env p	Adk14405 HIV mutan	Adx39690 HIV Env p		Aaw11581 Human Imm			Aab61505 HIV-1 SOS	Abr57052 HIV-1 JR-		Adk14399 HIV gp140	Adu22853 HIV-1 JR-
ADM73868	ABB06211	ADX39692	ADZ04164	AAR67724	ADK14406	ADP20081	ADK14404	ADX39677	ADX39681	ADK14405	ADX39690	ADX39676	AAW11581	AAW88113	ADX39674	AAB61505	ABR57052	ADF18107	ADK14399	ADU22853
80	Ŋ	σ	σ	~	œ	œ	œ	0	Ò	œ	σ	0	~	7	σ	4	ø	7	œ	80
842	842	843	842	850	847	847	847	856	856	847	791	855	855	855	855	643	643	643	643	643
82.8	82.6	82.6	82.5	82.1	82.0	82.0	81.9	81.9	81.9	81.9	81.8	81.6	81.6	81.6	81.5	81.4	81.4	81.4	81.4	81.4
2876.5	2870.5	2869.5	2867.5	2852	2849.5	2849.5	2845.5	2845	2844	2843.5	2840.5	2836.5	2834	2834	2831.5	2827.5	2827.5	2827.5	2827.5	2827.5
25	56	27	58	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

AAW44250 standard; protein; 649 AA. HIV-1 gp160 residues 33-681. (first entry) (revised) 17-OCT-2003 26-JUN-1998 AAW44250; AAW44250

Vaccine, antibody, antigen, hydrophobic; proteosome, pathogen, immune response, sexually transmitted disease, HIV; infection.

Human immunodeficiency virus 1.

491. .519 /note= "hydrophobic region" Location/Qualifiers 97WO-US012253. 96US-0021687P. (INTE-) INTELLIVAX INC. (JACK-) JACKSON FOUND HENRY (USSA) US SEC OF ARMY. WO9801558-A2 10-JUL-1997; 10-JUL-1996; 15-JAN-1998 Key Region

Birx DL; Vancott TC, Lowell GH,

Σ

WPI; 1998-110231/10.

Vaccine compositions for eliciting neutralising antibodies - comprising antigen containing hydrophobic sequence or having added hydrophobic material, complexed to proteosomes or bio-adhesive nano-emulsions.

Claim 9; Page 22; 62pp; English.

The present sequence represents HIV-1 gp160 residues 33-681 (the full protein is on the SWISS-PROT database Seq ID: 119434) used in a vaccine of the present invention. The vaccine composition is capable of eliciting neutralising antibodies in a subject to a pathogenic organism which antibodies are present in vaginal secretions, intestinal secretions, lung

gpl20 protein; purification; fractionation; ion exchange; chromatography; binding affinity; CD4; hydrophobic interaction; size exclusion; vaccine.

Human immunodeficiency virus 1.

US5696238-A

09-DEC-1997

91US-00684963. 93US-00109002. 94US-00240073.

16-AUG-1993

95US-00439286

11-MAY-1995; 20-AUG-1991; 09-MAY-1994;

HIV-1 gp120 protein fragment from isolate CDC4.

gp120

(first entry)

(revised)

17-OCT-2003 11-SEP-1998

AAW43072;

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NFN/MKNNWVAQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVW 120
                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                             360
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                                                                                                                                                                                                                                                                                                                          EQRGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSVI 180
                                                                                                                                                                                                                                                                                                                                                                                                     NGSLABEEVVIRSENFINNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIRCSSNITGLLITRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                          1 ANLWYTYTGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTE
                                                                                                                                                                                                                                                                                                                                                                            TQACPKVSFEDIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLL
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                                                                                                                                                                                                                                              1 ANLWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTE
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                                                                                                                                                                                                       Query Match 99.5%; Score 3457; DB 2; Length 649; Best Local Similarity 99.5%; Pred. No. 7.9e-187; Matches 646; Conservative 1; Mismatches 2; Indels (
                                                                                                                                                                                      Sequence 649 AA;
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Purification of HIV gp120 - using chromatographic methods

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Haigwood

Scandella C,

(CHIR) CHIRON CORP.

WPI; 1998-041353/04.

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immunodeficiency virus type I (HIV-1) isolates. These proteins are used in a novel method for purifying HIV gp120 so as to provide a purified gp120 glycopeptide having protein/protein binding properties gp120 glycopeptide having protein/protein binding properties substantially identical to natural viral HIV gp120. The method involves fractionating a crude gp120 preparation containing full-length, gp120 using ion exchange chromatography so as to provide a first collection of fractions. A a fraction from the first collection is selected that exhibits specific binding affinity for CD4 peptide, thereby producing a first fractionated material. The first fractionated material is fractionated by hydrophobic interaction chromatography so as to provide a second collection of fractions from which a second collection is selected that exhibits specific binding affinity for CD4 peptide. This second fraction is fractionated by size exclusion chromatography so as to provide a third collection of fractions exhibiting specific binding affinity for CD4 peptide. This affinity for CD4 peptide, thereby providing the purified gp120. The purified gp120 can be used for antibody production and in vaccines. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ANLWVIVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 ANLWYTVYYGVPVWKEA-TTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NFNWWXNNWVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTN-TTELSIIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 NENWAKONAWVEQMHEDIISLAMDQSLKPCVKLTPLCVTLNCTDLNTNNTTNSTTELSIIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 VITQACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQL
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Pred. No. 7.8e-183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 2A-W; 53pp; English.
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AAW43072 standard; peptide; 865

RESULT 2 AAW43072 ID AAW4

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                                                                                                                                                                      IKAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKT 598
                                                                                                                                                                                                               sednences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     that are determined founder sequences of a highly diverse viral strain, useful for diagnosing, preventing or treating viral (e.g. HIV) infection
                                                                                                                                                                                                                                                                                                                                                                                   Immune stimulation; diagnosis; gene therapy; viral infection; virucide; infection; HIV infection; anti-hiv; env protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an ancestral or center of tree (COT) viral nucleic acid and amino acid sequences that are determined founder sequences of a highly diverse viral strain. The invention also relates a composition comprising a highly diverse viral ancestor protein or an
                                                                                                                                 KGLIRCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT
                                                                                            - FYCNSTQLFNSAWNVTSNGTWSVTRKQKDTGDIITLPCRIKQ-INRWQVVGKAMYALPI
       LLINGSLAEEEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTG
                                                                                 PPYCNSTQLFNSAWNVTSNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYALPI
                                                                                                                       KGLIRCSSNITGLLITRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT
                                                                                                                                                          KAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated ancestral or COT viral nucleic acid and amino acid
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                                                                                                                                                                                                                                                                                                                                                                  protein, Bgp160.LScot, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WASHINGTON OFFICE TECHNOLOGY TRANSF.
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2001WO-US005288.
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                                                                                                                                                                                                                                                                                                        AEB10584 standard; protein;
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16-FEB-2001; 2
16-FEB-2001; 3
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immunogenic fragment of an ancestor or COT protein for inducing an immune response in a mammal and a method for preparing an ancestral or COT viral amino acid sequence. The composition and methods are useful for diagnosing, preventing or treating viral (e.g. HIV) infection. The invention is also useful in gene therapy. The present sequence is a clade most recent common ancestor (MRCA), COT least squares (LScot) and COT minimum of means (MMCot) reconstructions for the clade B env gene.
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                                                                                                                                                                                                                                                                                                          LWVIYYGVPVWKEAITTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLENVTENF
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                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                           ; Score 2987; DB 9;
; Pred. No. 3.1e-160;
31; Mismatches 46;
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Best Local Similarity 86.6%;
Marches 563; Conservative
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(first entry)
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29-OCT-2001
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ADW38347 standard; protein; 883
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Human immunodeficiency virus 1.
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Best Local Similarity 84.77
Matches 564; Conservative
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FNCGGEFFYCNSTQLFNSTWHF--NGTWGNNNTERSNNAADDNDTITLPCRIKQIINMWQ 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus (FIV) nucleic acid sequence or its fragment is a determined founder sequence of a highly diverse viral strain, subtype or group. Also described are: an isolated ancestor protein or its fragment from FIV; an isolated expression construct comprising the operably linked elements consisting of a transcriptional promoter, a nucleic acid encoding an FIV ancestor protein and a transcriptional terminator; a cultured prokaryotic
YTTGEILGNIRQAHCNISRAQWNNTLQQIATTLREQFGNK--TIAFNQSSGGDPEIVMHS 352
                                                                                                                                              407
                                                                                                                                                                                                                                                                                            463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARVLAVERYLKDQQLLGIWGCSGKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTAVPWNASHSNKSLDKIWNNMTWMEWEREIDNYTGLIYTLIEESQNQQEKNEQELLEL
                                                                                                                                              FNCGGEFFYCNSTQLFNSAMNVTSNGTWSVTRKQK-----DTGDIITLPCRIKQIINRWQ
                                                                                                                                                                                                                                                                                        VVGKAMYALPIKGLIRCSSNITGLLLTRDGGGENQT----TEIFRPGGGDMRDNWRSELY
                                                                                                                                                                                                                                                                                                                                                        EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNENTNNTDTEIFRPGGGDMRDNWRSELY
                                                                                                                                                                                                                                                                                                                                                                                                                                   KYKVVKI EPLGVAPTKAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLSGIVQQQNNLLRAIKAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis; FIV infection; envelope; env.
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group M, subtype B, ancestral envelope protein (env).

19-MAY-2005 (first entry)

HIV-1

or eukaryotic cell transformed or transfected with the expression construct; a composition for inducing an immune response in a mammal comprising a highly diverse FIV ancestor protein or its antigenic fragment; a method of preparing an FIV viral amino acid sequence; a method for inducing an immune response to FIV in a host; a method for making an PIV vaccine; a kit comprising a composition comprising an ancestor protein or an antigenic fragment of an FIV ancestor protein and instructions for administering the composition to a subject; and a method for detecting infection with FIV. The ancestral feline immunodeficiency virus (FIV) nucleic acid sequence is useful in preparing a vaccine against FIV. This is the amino acid sequence of ancestral HIV-1 group M subtype B envelope (env) protein. 8 \times 9 \times 9

Sequence 883 AA;

NAMYNNWVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWEQ 122 RG-----KGEMRNCSFNITTSIRDKVQREYALFYKLDVEPID-DNKNTTNNTKYRLIN 174 153 SGGTWEGEKGEIKNCSFNVTTSIRDKMQKEYALFYKLDVVPIDNDNNNTNNNTSYRLIN 212 CNTSVITQACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVV 234 STQLLLINGSLABEEVVIRSENFINNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVW 294 YTTGEILGNIRQAHCNISRAQWNNTLQQIATTLREQFGNK--TIAFNQSSGGDPEIVWHS 352 FNCGGEFFYCNSTOLFNSTWHF -- NGTWGNNNTERSNNAADDNDTITLPCRIKQIINWWQ 450 463 510 523 630 643 690 YATGKIIGDIRQAHCNLSRAKWNNTLKQIVTKLREQFGNNKTTIVFNQSSGGDPEIVWHS 392 FNCGGEFFYCNSTQLFNSAWNVTSNGTWSVTRKQK----DTGDIITLPCRIKQIINRWQ 407 62 92 3 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF LWVIVYYGVPVWKEATITILFCASDAKAYDIEVHNVWATHACVPIDPNPOEVVLENVTENF 213 CNTSVITQACPKVSFEPIPIHYCTPAGFAILKCNDKKFNGTGPCTNVSTVQCTHGIRPVV VVGKAMYALPIKGLIRCSSNITGLLLTRDGGGENQT----TEIFRPGGGDMRDNWRSELY EVGKAMYAPPISGQIRCSSNITGLLITRDGGNNENTNNTDTRIFRPGGGDMRDNWRSELY KYKVVKIEPLGVAPTKAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQ CTTAVPWNASWSNKTLDQIWNNMTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQL CTTAVPWNASWSNKSLDKIWNNWTWMEWEREIDNYTGLIYTLIEESQNQQEKNEGELLEL LLSGIVQQQNNLLRAIKAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLI Gaps 21; 85.7%; Score 2977.5; DB 9; Length 883; 84.7%; Pred. No. 1.1e-159; ive 27; Mismatches 54; Indels 21; Matches 564; Conservative 969 DKWASL 649 Best Local Similarity DKWASL 6 33 63 93 123 273 333 393 408 451 511 571 631 644 Query Match 175 235 292 353 464 584 691 ઠે g ð 셤 ò 셤 8 ద δ g g ò g 셤 ò 셤 ઠે 셤 ò ठे ð ð

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sequence and its fragment, where the sequence is a determined founder sequence of a highly diverse viral strain, subtype or group of an endogenous retrovirus. Also included are an isolated ancestor protein (or its fragment) from an endogenous retrovirus, an isolated expression construct (comprising the following operably linked elements: - a construct (comprising the following operably linked elements: - a construct (comprising the following operably linked elements: - a correction and a transformed or transfected with the protein construct, a composition for inducing an immune response in a recipient construct, a composition for inducing an immune response in a recipient construct, a composition for inducing an immune response in a recipient construct, a composition for inducing an immune response in a recipient construct, a binds specifically to an endogenous retrovirus ancestor protein (and that binds specifically to a plurality of circulating descendant endogenous retrovirus ancestor proteins), a method of corporating an ancestral endogenous retrovirus anno acid sequence, a method for inducing an immune response to a donor virus in a transplant recipient or a potential transplant recipient, a method of matking a construct or a preparing an endogenous retrovirus an endogenous retrovirus and end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factors commonly associated with viral activation, e.g. immune suppression, graft versus host disease, graft rejection, viral co-infection, and cytotoxic therapies. The present sequence is an ancestral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viral infection in transplantation that is heightened by the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated ancestral viral nucleic acid sequence that is a determined founder sequence of a highly diverse viral strain, subtype or group of endogenous retrovirus, useful in the prophylaxis of viral infection.
                                                                                                                                            Xenotransplantation; vaccine; acquired immune deficiency syndrome; anti-hiv; immune disorder; HIV-1 infection; infection; PERV infection; diagnosis; graft versus host disease; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated ancestral viral nucleic acid
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                                                                                                                                                                                                                                                                                              Human immunodeficiency virus 1; subtype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROBS HA;
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                                                                                                                                                                                                                                        envelope protein.
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                                                                                                                                                                                                                                                                                                                          Synthetic.
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9

Gaps

21;

Indels

Query Match

85.7%; Score 2977.5; DB 9;
Best Local Similarity 84.7%; Pred. No. 1.1e-159;
Matches 564; Conservative 27; Mismatches. 54;

ADY27998 standard; protein; 883 AA.

9 RESULT

ADY27998

Length 883;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stimulation; diagnosis; gene therapy; viral infection; virucide; on; HIV infection; anti-hiv; ancestor protein.
                                NMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWEQ
                                         CNTSVITQACPKVSFEPIPIHYCTPAGFAILKCNDKKFNGTGPCTNVSTVQCTHGIRPVV
                                                                                                                                                           YTTGEILGNIRQAHCNISRAQWNNTLQOIATTLREQFGNK--TIAFNQSSGGDBEIVMHS
                                                                                                                                                                    KYKVVKIEPLGVAPTKAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGAASMTLTVQARQ
         LWVIVYYGVPVWKEAITILFCASDAKAYDTEVHNVWAIHACVPIDPNPOEVVLENVTENF
                                                               RG-----KGEMRNCSFNITTSIRDKVQREYALFYKLDVEPID-DNKNTTNNTKYRLIN
                                                                                             CNTSVITQACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVV
                                                                                                                                                                                          FNCGGEFFYCNSTQLFNSAWNVTSNGTWSVTRKQK----DTGDIITLPCRIKQIINRWQ
                                                                                                                                                                                                        FNCGGEFFYCNSTQLFNSTWHF -- NGTWGNNNTERSNNAADDNDTITLPCRIKQIINMWQ
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 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF
                                                                                                                                                                                                                        VVGKAMYALPIKGLIRCSSNITGLLLTRDGGGENQT----TEIFRPGGGDMRDNWRSELY
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2000US-0183659F. 2001US-00204204. 2001WO-US005288.

18-FEB-2000; 16-FEB-2001; 16-FEB-2001;

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The invention relates to an ancestral or center of tree (COT) viral nucleic acid and amino acid sequences that are determined founder sequences of a highly diverse viral strain. The invention also relates to a composition comprising a highly diverse viral ancestor protein or an immunogenic fragment of an ancestor or COT protein for inducing an immune response in a mammal and a method for preparing an ancestral or COT viral amino acid sequence. The composition and methods are useful for diagnosing, preventing or treating viral (e.g. HIV) infection. The invention is also useful in gene therapy. The present sequence is an ANI-
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                                               TECHNOLOGY
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14-FEB-2003; 2003US-0447586P
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Best Local Similarity 84.7<sup>7</sup>
Matches 564; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EnvB ancestor protein.
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STOLLLINGSLABEEVVIRSENFINNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVW 294
                                                                                                                      anti-HIV; Immunostimulant; immune stimulation; HIV infection; infection;
                                                    CNTSVITQACPKVSFEPIPIHYCTPAGFAILKCNDKKFNGTGPCTNVSTVQCTHGIRPVV
                                                                                                                                                                                           333 YATGKIIGDIRQAHCNLSRAKWNNTLKQIVTKLREQFGNNKTTIVFNQSSGGDPEIVWHS
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SGGGTMEGEKGEIKNCSFNVTTSIRDKMQKEYALFYKLDVVPIDNDNNNTNNNTSYRLIN
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                                                                                                                                                                                                                                                                                                              408 VVGKAMYALPIKGLIRCSSNITGLLLTRDGGGENQT----TEIFRPGGGDMRDNWRSELY
                                                                                                                                                                                                                                                                                                                                              451 EVGKAMYAPPISGQIRCSSNITGLLLTRDGGNNENTNNTDTEIFRPGGGDMRDNWRSELY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-2003; 2003US-0503460P.
27-AUG-2004; 2004US-0604722P.
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Gao F, Liao H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KORBER B T.
HAHN B H.
SHAW G M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKWASL 649
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LI Y Y.
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(HAHN/)
(SHAW/)
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(LIYY/)
(DECK/)
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Haynes |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated ancestral or COT viral nucleic acid and amino acid sequences that are determined founder sequences of a highly diverse viral strain, useful for diagnosing, preventing or treating viral (e.g. HIV) infection.
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                                                                                                                                                                                                                                                                                            therapy; viral infection; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KGEMENCSFNITTSIRDKVQREYALFYKLDVBPID-DNKNTTNNTKYRLIN
CTTAVPWNASWSNKSLDKIWNNWTWMEWEREIDNYTGLIYTLIEESQNQQEKNEQELLEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jensen MA;
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                                                                                                                                                                                                                                                                                          Immune stimulation, diagnosis, gene therapy, viral infect
infection, HIV infection, anti-hiv, env ancestor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Learn GH, Li F, Nickle DC,
                                                                                                                                                                                                                                                           SEQ ID NO: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.7%; Score 2977.5; DB 9; 84.7%; Pred. No. 1.1e-159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNIW ) UNIV WASHINGTON OFFICE TECHNOLOGY TRANSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564; Conservative, 27; Mismatches
                                                                                                                                                                                                                                                             env ancestor protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID NO 2; 201pp; English
                                                                                                                                                     AEB10552 standard; protein; 883 AA.
                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001US-00204204.
2001WO-US005288.
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N-PSDB; AEB10551.
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Best Local Similarity
                                                                                                                                                                                                                                                           HIV-1, subtype B,
                                                                                                                                                                                                                                                                                                                                                                                  US2005137387-A1.
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                                DKWASL
                                                              DKWASL
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Matches
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The invention describes an isolated protein (I) selected from 106 fully defined 500-866 amino acid sequences given in the specification. Also described are: a nucleic acid comprising: a nucleotide sequence encoding COMG HIV gp160 protein, subtype C ancestral HIV envelope protein, subtype C consensus HIV envelope protein, subtype C consensus HIV net protein, Group M consensus HIV envelope protein, subtype A consensus HIV pol protein, Group M consensus HIV of protein, subtype A consensus HIV pol protein, Group M consensus HIV of protein, subtype C consensus HIV pol protein, subtype B consensus HIV gag protein, or subtype B consensus HIV pol protein, subtype B consensus HIV gag protein, or subtype C consensus HIV pol protein, subtype B consensus HIV gag protein, or subtype B consensus HIV pol protein, subtype B consensus HIV gag protein, or subtype B consensus HIV gag protein, a vector comprising the nucleotide sequence comprising the nucleotide sequence encoding (I); or a nucleotide sequence specification; a vector comprising the nucleic acid of (I); a composition comprising at least one protein or nucleic acid above and a carrier; and consensus in mammal. The protein is a consensus or consensus or ancestral immunogen useful for inducing antinuose a T cell response. This is the amino acid sequence of HIV subtype B consensus env protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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                                                                       New isolated consensus or ancestral immunogenic proteins, useful for inducing antibodies that neutralize a wide spectrum of human immunodeficiency virus (HIV) primary isolates and/or that induces a T
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                                                                                                                                                                     Example 7; Fig 20D; 284pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562; Conservative
               2005-242571/25
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                                     N-PSDB; ADZ07747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 850 AA;
                                                                                                                                  cell response
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an ancestral or center of tree (COT) viral nucleic acid and amino acid sequences that are determined founder sequences of a highly diverse viral strain. The invention also relates to a composition comprising a highly diverse viral ancestor protein or an immunogenic fragment of an ancestor or COT protein for inducing an immune response in a mammal and a method for preparing an ancestral or COT viral diagnosing, preventing or treating viral (e.g. HIV) infection. The diagnosing is also useful in gene therapy. The present sequence is a clade B env (gp160) protein. This sequence is used in the comparison of the most recent common ancestor (MRCA), COT least squares (LSCOt) and COT minimum of means (MMCC) reconstructions for the clade B env gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FINAWKONNYVEQWHEDIISLWDQSLKPCVXLTPLCVTLACTDLATINTTRTTTLSIIVVWE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated ancestral or COT viral nucleic acid and amino acid sequences that are determined founder sequences of a highly diverse viral strain, useful for diagnosing, preventing or treating viral (e.g. HIV) infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                                                    Immune stimulation; diagnosis; gene therapy; viral infection; virucide; infection; HIV infection; anti-hiv; env protein.
543 QHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVFWNASWSNKTLDQI
                 32 NLWYTVYYGVPVWKRATTTLFCASDAKAYKTEVHNVWATHACVFTDPNPQEVVLENVTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NLWVTVYYGVPVWKEALTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li F, Nickle DC, Jensen MA;
                                                                   649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.9%; Score 2949; DB 9; Length 862; 85.6%; Pred. No. 4.3e-158; ive 32; Mismatches 52; Indels 10
                                                                 603 WNNMTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQLDKWASL
                                                                                  Bgp160.mrca, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNIW ) UNIV WASHINGTON OFFICE TECHNOLOGY TRANSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID NO 50; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mullins JI, Rodrigo AG, Learn GH,
                                                                                                                                                                                   Ä
                                                                                                                                                                                 AEB10583 standard; protein; 862
                                                                                                                                                                                                                                                                                     protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-00204204.
2001WO-US005288.
2003US-0447586P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0183659P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 85.6%
Matches 557; Conservative
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-444181/45.
N-PSDB; AEB10560.
                                                                                                                                                                                                                                                                                   Clade B env (gp160)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-2001;
16-FEB-2001;
14-FEB-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2000;
                                                                                                                                                                                                                                                  25-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                557
                                                                                                                                                                                                                  AEB10583;
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                          QRGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSVIT
                                        TWEKGEMKNCSFNITTSIRDKWOKEYALFYKLDVVPIDNDNNSNNNTNYRLINCNTSVIT
                                                                            QACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLN
                                                                                           QACPKVSFEPIPIHYCTPAGFAILKCNDKKFNGTGPCKNVSTVQCTHGIRPVVSTQLLLN
                                                                                                                                GSLAEEEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEIL
                                                                                                                                               GSLAEBEEVVIRSENFIDNAKTIIVOLMESVEINCTRPNNNTRKSIPIGPGRALYTGEII
                                                                                                                                                                                     GNIROAHCNISRAQWNNTLQQIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEFF
                                                                                                                                                                                                        GDIRÓAHCNISRAKWANTLKQVVTKLREQFGNNKTIVFNPSSGGDPEIVMHSFNCGGFF
                                                                                                                                                                                                                                        YCNSTQLFNSAWNVTSNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYALPIKG
                                                                                                                                                                                                                                                                 YCNTTOLFNSTWNST-EGSNKTTGSNNTGGETITLPCRIKQIINMWQEVGKAMYAPPIRG
                                                                                                                                                                                                                                                                                             LIRCSSNITGLLLTRDGGGENOT - - TEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT
                                                                                                                                                                                                                                                                                                                    OIKCSSNITGLLLTRD-GGENSTNETEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT
                                                                                                                                                                                                                                                                                                                                                KAKRRVVOREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVOAROLLSGIVQQQNNLLRA
                                                                                                                                                                                                                                                                                                                                                               IKAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant modified vaccinia Ankara virus comprising first null
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infectious disease; HIV; hepatitis; variola virus infection;
immune stimulation; antimicrobial; virucide; anti-HIV; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDKIWNNMTWMEWEREIDNYTGLIYNLIEESQNQQEKNEQELLELDKWASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viral replication; recombinant DNA; vector; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human codon-optmized HIV B Env protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADY99903 standard; protein; 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus 1.
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virus (rWWA). Specifically, it refers to the use of rWA vectors in the development of vaccines to protect against cancer or infectious viral diseases such as HIV, hepatitis and smalpox. The present invention of searches introducing a neutral multiple describes introducing a neutral multiple describes introducing a neutral multiple describes introducing a necessary for replication of the rWVA, in particular an exemplary gene is the vaccinia uracil DNA givosylase gene. Additional vaccinia genes that can contain null mutations include, but are not limited to, ILI beta receptor, A46R, IL-18BP, A41L and B31.

Accordingly, it provides a system for producing an appropriate vaccine that involves an immortalized, non-transformed avian fibroblast cell infected with the rMVA, where the cell is from a complementing cell line that include an interpretation of that the virus is able to propagate. Purthermore, the rMVA may include a heterologous nucleic acid sequence encoding an antigen or a fragment thereof derived from viral, animal or plant polynucleotides, for example this may include an antigen from the HIV virus, massales virus, sand mutagen from the river blindness nematode.

The rMVA also comprises a second heterologous nucleic acid sequence or an antigen or a mutagen from the river blindness nematode.

The rMVA also comprises a second heterologous nucleic acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in a host and exhibits antimicrobial, virucide, anti-HIV, cytostatic, antiinflammatory and hepatocropic activities. This polypeptide sequence is a human codon-optimized HIV-1 consensus protein sequence, encoded by an antigenic sequence of an MVA-based vector given in an exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linked to an early stage viral promoter. As such, the developed vaccine can be administered in a sufficient amount to effect an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding a pro-apoptotic, anti-apoptotic or an immunomodulator operably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAWKONNAVEOMHEDIISLWDQSLKPCVKLTPLCVTLNCTDL--RNATNTTSSS----WET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSVITQ
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preventing viral cancer.
                                                                                                   to a novel recombinant modified vaccinia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
mutation in vaccinia gene, useful for treating or infection (e.g. HIV, hepatitis and smallpox), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2947; DB 9;
Pred. No. 5.4e-158;
; Mismatches 40;
                                                          69; SEQ ID NO 31; 324pp; English
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86.2%;
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                                                                                                   invention relates
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                                                            Claim
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RVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLRAIKAQ 542

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RCSSNITGLLLTRDGGKDTNGTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR

RCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR

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This invention telates to a mover accomplaint modulities vaccinia Antwara virus (TWMA). Specifically, it refers to the use of rWMA vectors in the development of vaccines to protect against cancer or infectious viral development of vaccines to protect against cancer or infectious viral development as HIV, hepatitis and smallpox. The present invention describes introducing a mull mutation (preferably a deletion) into a vaccinia gene that is necessary for replication of the rWWA, in the constitution of the rWWA, in the constitution of the rWMA, in the constitution of the rWMA, in the constitution of the rWMA, in the constitution of the rWMA in the result of the rWMA where the contain null mutations include, but are not limited to, Ill beta receptor, A46R, IL-18BP, A41L and E31.

Accordingly, it provides a system for producing an appropriate vaccine that involves an immortalized, non-transformed avian fibroblast cell infected with the rWWA, where the cell is from a complementing cell line that involves an immortalized, non-transformed avian fibroblast cell include a heterologous nucleic acid sequence encoding an antigen or a fragment thereof derived from viral, animal or plant polynuclectides, can mutate or the river blindness nematode. SARS virus, influence a second heterologous nucleic acid sequence can example this may include an antigen from the HIV virus, measles virus, sample this may include an antigen from the HIV virus, measles virus, can antigen from the river blindness nematode. The rMWA also comprises a second heterologous nucleic acid sequence encoding a pro-apoptotic, anti-apoptotic or an immunomodulator operably linked to an early stage viral promoter. As such, the developed vaccine
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QHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKTLDQI
                                                                                                                                                      invention relates to a novel recombinant modified vaccinia Ankara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; cancer; infectious disease; HIV; hepatitis; variola virus infection; immune stimulation; antimicrobial; virucide; anti-HIV; cytostatic; antinflammatory; hepatotropic; immunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nef; fusion protein; viral replication; recombinant DNA; vector;
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                                                                                                                                                                                                                                                                                                      WNNMTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQLDKWASL 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human codon-optmized HIV B Env-Nef fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADY99925 standard; protein; 1068
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can be administered in a sufficient amount to effect an immune response in a host and exhibits antimicrobial, virucide, anti-HIV, cytostatic, antiflammatory and hepatotropic activities. This polypeptide sequence is a human codon-optimized HIV-1 consensus fusion protein sequence, encoded by an antigenic sequence of an MVA-based vector given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gag; pol; env; nef; fusion protein; viral replication; recombinant DNA; vector; vaccine; cancer; infections disease; HIV; hepatitis; variola virus infection; immune stimulation; antimicrobial; virucide; anti-HIV; cytostatic; antiniflammatory; hepatotropic; immunogenicity.
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                                                                                                                                               Gaps
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                                                                                                                   Length 1068;
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; Mismatches 40;
                                                                                                                   DB 9;
                                                                                                                   84.8%; Score 2947;
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                                                                                                                             Best Local Similarity 86.2
Matches 558; Conservative
                                                                                          Sequence 1068 AA;
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                                                                    anti-HIV; Immunostimulant; immune stimulation; HIV infection; infection; CON-B; env; envelope; fusion protein.
                                                                                                                                                                                                                                                        2024 RVVQREKRAVG-IGAMFLGFLGAAGSTMGAASMTLTVQARQLLSGIVQQQNNLLRAIEAQ
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                                            SLAEBEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEILG
                                                                                                                                                                                                                            NSTQLFNSAWNVTSNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYALPIKGLI
                                                                                                                                                                                                                                                                                                                   423 RCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2143 WINMTWMEWEREIDNYTSLIYTLIEBSQNQQEKNEQELLELDKWASL 2189
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27-AUG-2004; 2004US-0604722P.
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KORBER B T.
HAHN B H.
SHAW G M.
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DECKER J.
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Haynes BF,
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Accordingly, it provides a system for producing an appropriate vaccine that involves an immortalized, non-transformed avian fibroblast cell infected with the rWMA, where the cell is from a complementing cell line that the virus is able to propagate. Furthermore, the rMM may cinclude a heterologous nucleic acid sequence encoding an antigen or a fragment thereof derived from viral, animal or plant polynucleotides, for example this may include an antigen from the HIV virus, measles virus, SARS virus, influenza virus, malaria plasmodium, tuberculosis Bacillus, yellow fever virus, dengue flavivirus or the river blindness menatode.

The rMMA also comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding a pro-apoptotic, anti-apoptotic or an immunomodulator operably linked to an early stage viral promoter. As such, the developed vaccine can be administered in a sufficient amount to effect an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in a host and exhibits antimicrobial, virucide, anti-HIV, cytostatic, antiinflammatory and hepatotropic activities. This polypeptide sequence is a human codon-optimized HIV-1 consensus fusion protein sequence, encoded by an antigenic sequence of an WVA-based vector given in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to a novel recombinant modified vaccinia Ankara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1627 NAWKNNWVEOMHEDIISLWDOSLKPCVKLTPLCVTLNCTDL--RNATNTTSSS----WET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTINNIKYRLINCNISVITQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1567 LWVTVYYGVPVWKEATTTLFCASDAKAYDTBVHNVWATHACVPTDPNPQEVVLENVTENF
                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant modified vaccinia Ankara virus comprising first null, mutation in vaccinia gene, useful for treating or preventing viral infection (e.g. HIV, hepatitis and smallpox), and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.8%; Score 2947; DB 9; Length 2602;
86.2%; Pred. No. 1.4e-157;
ive 25; Mismatches 40; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 69; SEQ ID NO 57; 324pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the invention
                Human immunodeficiency virus 1.
                                                                                                                                                      20-SEP-2004; 2004WO-US030849.
                                                                                                                                                                                                  18-SEP-2003; 2003US-0504030P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 86.2
Matches 558; Conservative
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                                                                                                                                                                                                                                                                                            Garber
                                                                                                                                                                                                                                                                                                                                        WPI; 2005-254126/26.
                                                                                                                                                                                                                                             (UYEM-) UNIV EMORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2602 AA;
                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADY99928
                                                               WO2005028634-A2
                                                                                                                                                                                                                                                                                            Feinberg MMD,
sapiens
                                                                                                            31-MAR-2005
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The invention describes an isolated protein (I) selected from 106 fully defined 500-866 amino acid sequences given in the specification. Also described are: a nucleic acid comprising: a nucleotide sequence encoding CONG HIV gp160 protein, subtype C ancestral HIV envelope protein, subtype C consensus HIV envelope protein, subtype C consensus HIV nef protein, Group M consensus HIV envelope protein, subtype A consensus HIV envelope protein, Group M consensus HIV or gag protein, subtype C consensus HIV pol protein, Group M consensus HIV or gag protein, or subtype C consensus HIV pol protein, subtype B consensus HIV envelope protein, where the conclectide sequence comprises codons optimized for expression in human cells; a nucleotide sequence encoding (I); or a nucleotide sequence comprising the nucleotide sequence encoding (I); or a nucleotide sequence comprising the nucleotide sequence comprising the nucleic acid above and a carrier; and inducing at least one protein or nucleic acid above and a carrier; and inducing an immune response in a mammal. The protein is a consensus or ancestral immunogen useful for inducing antiduces at cell response. This is the amino acid sequence of a HIV (CON-B) consensus gp140 env
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NWWKNNNVEQWHEDIISLWDQSLKPCVKLTPLCVTLNCTDLMNATNTTT---IIYRW-- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSVITQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --RGEIKNCSFNITTSIRDKVQKEYALFYKLDVVPIDN----DNTSYRLISCNTSVITQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLAEEEVVIRSENFINNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEILG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLRAIKAQ 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 SLAEEEVVIRSENFIDNAKTIIVQLNESVEINCTRPNNNTRKSIHIGPGRAFYTTGEIIG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSTQLFNSAWNVTSNGTWSVTRKQKDTGDIJTLPCRIKQIINRWQVVGKAMYALPIKGLI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 NTTQLFNSTW----NGTWN-----NTEGNITLPCRIKQIINMWQEVGKAMYAPPIRGQI 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLENVTENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIROAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGEFFYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKTLDQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9; Length 841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WNNMTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQLDKWASL 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.6%; Score 2939.5; DB 9; 86.1%; Pred. No. 1.4e-157; ive 31; Mismatches 34;
Disclosure; Fig 28A; 284pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity 86.1
557; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 841 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    fusion protein
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Best Local S
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The invention describes an isolated protein (I) selected from 106 fully defined 500-866 amino acid sequences given in the specification. Also described are: a nucleic acid comprising: a nucleotide sequence encoding COM6 HIV gpl60 protein, subtype C ancestral HIV envelope protein, subtype C consensus HIV net protein, group M consensus HIV envelope protein, subtype C consensus HIV envelope protein, group M consensus HIV gag protein, subtype A consensus HIV pol protein, group M consensus HIV gag protein, subtype B consensus HIV pol protein, subtype B consensus HIV pol protein, subtype B consensus HIV pol protein, subtype B consensus HIV gag protein, subtype B consensus HIV envelope protein, where the nucleotide sequence comprises codons optimized for expression in human cells; a nucleotide sequence encoding (I); or a nucleotide sequence comprising the nucleic acid above and a carrier; and inducing an immune response in a mammal. The protein is a consensus or ancestral immunogen useful for inducing antihucing an immune seponse in a mammal. The protein is a consensus or ancestral immunogen useful for inducing antihodies that neutralize a wide spectrum of HIV primary isolates and/or that induces a T cell response. This is the amino acid sequence of HIV (CON-B) envy protein.
                                                                                                                                                anti-HIV; Immunostimulant; immune stimulation; HIV infection; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated consensus or ancestral immunogenic proteins, useful for inducing antibodies that neutralize a wide spectrum of human immunodeficiency virus (HIV) primary isolates and/or that induces a T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Decker J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li YY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kothe D,
ADZ07794 standard; protein; 841 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 66; Fig 44A; 284pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shaw GM,
Liao H;
                                                                                                                                                                                                      Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                    17-SEP-2004; 2004WO-US030397
                                                                                                                                                                                                                                                                                                                                                         17-SEP-2003; 2003US-0503460P
                                                                                                                                                                                                                                                                                                                                                                        27-AUG-2004; 2004US-0604722P
                                                                         (first entry)
                                                                                                             HIV CON-B env protein.
                                                                                                                                                                     CON-B; env; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hahn BH,
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KORBER B T.
HAHN B H.
SHAW G M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell response.
                                                                         16-JUN-2005
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                                    ADZ07794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DECK/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Korber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Наупев
                                                                                                                                                                                                                                                                                                                                                                                                                                  (KORB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HAHN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHAW/)
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7; 62

25;

35; Indels

tch 84.3%; Score 2927.5; DB 9. al Similarity 85.9%; Pred. No. 6.8e-157; 556; Conservative 31; Mismatches 35;

Query Match Best Local Similarity

Matches

à

DB 9; Length 841;

3 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF

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182
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                                                                               --RGEIKNCSFNITTSIRDKVQKEYALFYKLDVVPIDN----DNTSYRLISCNTSVITQ 200
                                                                                                                      SLAEBEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEILG 302
                                                                                                                                                                                       NIRQAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGEFFYC 362
                                                                                                                                                                                                                              NSTQLFNSAWNVTSNGTWSVTRKQKDTGDIJTLPCRIKQIINRWQVVGKAMYALPIKGLI 422
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                              NAMININAVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWEQ 122
                                                                                                                                                                                                                                                                                                                                                                        607
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RGKGEMRNCS PNITTS I RDKVQREYAL FYKLDVEPI DDNKNTTNNTKYRLINCNTSVITQ
                                                                                                            ACPKVSFEP1P1HYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG
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1 ANLWVTVYYGVPVWKEATTT.....QNQQEKNQQELLQLDKWASL 649 US-09-938-406-i_COPY_33_681 3474 Perfect score: Scoring table: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* *:08 PIR Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

env protein - huma env polyprotein - env polyprotein pr envelope polyprotein pr env polyprotein env polyprotein pr
env polyprotein pr
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env protein - huma env polyprotein prenvelop glycoprote env polyprotein -env polyprotein P env polyprotein P Description SUMMARIES H44001 VCLJ3W T12016 S13289 VCLJAR VCLJAR VCLJYR VCLJY V A44963 T01672 VCLJSI A40218 S31493 C41621 VCLJH4 Query Match Length DB 80.9 80.8 80.8 80.8 80.6 80.5 80.1 779.6 773.3 773.9 773.9 773.9 2869.5 2858 2849.5 2837 2816.5 2816.5 2815.5 2809.5 2808 2808 2806.5 2799.5 2795 2782 2765.5 2746 2623.5 2616.5 2566 Score Š. Result

gag polyprotein -	envelope polyprote	env polyprotein pr	env protein - huma	env polyprotein pr	env polyprotein pr	env polyprotein pr	env polyprotein -	env polyprotein pr	envelope polyprote	env protein - huma	env polyprotein -	env polyprotein -	envelope polyprote	env polyprotein -	envelope polyprote
A53034	860538	VCLJST	S25940	VCLJS4	VCLJG2	VCLJGG	C46356	VCLJCT	853098	803068	VCLJG4	S04322	S60545	VCLJG3	S60548
7	N	-	~	н	ч	н	~	~	~	ď	н	7	~	~	77
863	297	823	290	712	828	852	877	859	869	881	864	882	294	881	301
49.0	34.7	34.1	33.9	33.6	33.5	33.3	33.1	32.8	32.7	32.6	32.6	32.5	32.5	32.5	32.4
1701.5	1204	1183.5	1176	1168.5	1164.5	1157	1150.5	1140	1135.5	1134	1133.5	1130	1129.5	1127.5	1127
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT VCLJH4 env pol	RESULT 1 VCLJH4 Polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)
N;Alternate N;Contains: C;Species: P C;Date: 30-C	N/Alternate names: coat polyprotein N/Contains: coat protein gp120; coat protein gp41 C:Species: human immunodeficiency virus type 1, HIV-1 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C, Acces R, Desai	С;Ассеввіоп: C25523 R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, А.; Andersen, Р.R.; Devare,
Proc. PA;Title	Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986 A.Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human
A; Reres	A;Recession (25523)
A;Resic	AjMOLECULE LYPE: DNA Afresidues 1-868 ADES. A Arcel-reference HITTEDOR DAEDO. INTENDATIONALISMAIL CE.M1313. MIT. 235660. DIEM.
C;Genetics:	Corresponding (Figures)
A;Gene: C;Superf	Ajene: env C;Superfamily: type E retrovirus env polyprotein
C; Keywo F;1-521	C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote F;1-521/Product: coat protein qp120 #status predicted <gp1></gp1>
F;522-E F;89,13	F;522-868/Product: coat protein gp41 #status predicted <gp2> F;89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459</gp2>
Query Ma Best Loc	Query Match 100.0%; Score 3474; DB 1; Length 868; Best Local Similarity 100.0%; Pred. No. 6.4e-247; Marches 649: Conservative 0. Mismatches 0. Indels 0. Gans 0.
ò	1 ANLWYTVYYGVPVWKEATTTLFCASDAKAYDTBAHNVWATHACVPTNPNPQEVVLENVTE 60
q	33 ANLWYTYYYGVPVWKEATTTLFCASDAKAYDTEAHNYWATHACVPTNFNPQEVVLENVTE 92
ò	61 NFNMWKNNMVEQMHEDIISLMDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVW 120
qq	93 NFNNWKNNWVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTHTTHTTHTH
ò	121 EQRGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKWTTNNTKYRLINCNTSVI 180
qq	픋
È	181 TQACPKVSFBIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLL 240
qq	213 TQACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLL 272
ò	241 NGSLAEBEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEI 300
qq	273 NGSLAEBEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVMYTTGEI 332

301 333

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env polyprotein P env polyprotein M envelope protein p env polyprotein D

1909 1825 1802 1751.5

Db 260 SLAEEBIVIRSENFTRNAKTIIVQLNESVVINCTRPNNNTRKSINIGPGRALYTTGEIIG 319 303 NIRQAHCRISRAQWINTLQQIATTLREQFG-NKTIAFNQSGGDPEIVMHSFNCGGEFFY 361 310 DIRQAHCRISRAQWINTLGQIATTLREQFG-NKTIAFNQSGGDPEIVMHSFNCGGEFFY 379 362 CNSTQLFNSAWNVTSNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAWYALPIKGL 421 380 CNSTQLFNSAWNVTSNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAWYALPIKGL 429 422 IRCSSNITGLLITRDGGGENQTTEIFRPGGGDWRDNWRSELYKKKVVKIEPLGVAPTKAK 481 430 IRCSSNITGLLITRDGGCENQTTEIFRPGGGDWRDNWRSELYKKKVVKIEPLGVAPTKAK 489 482 RRVVQREKRAVGMLGAMFLGFLGAAGSTWGATSMALTVQARQLLSGIVQQQNNLLRAIKA 541 430 RRVVQREKRAVG-LGALFLGFLGAAGSTWGATSMALTVQARQLLSGIVQQQNNLLRAIKA 541 649 RRVVQREKRAVG-LGALFLGFLGAAGSTWGATSMALTVQARQLLSGIVQQQNNLLRAIRA 548 672 QQHLLQLTVWGIKQLQARLLAAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSKTLDQ 601	609 IWDNMTWMKWEREIDNYTHIIYILIESSQNQOGENOCENOCENTRANSEL 649 [11.11	OY 63 NWWKNNWYBOWHEDIISLWDOSLKPCVYLAKTDLATNNTTELSIIVWEG 122
Oy 361 YCNSTQLFNSAWNVTSNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYALPIKG 420 193 YCNSTQLFNSAWNVTSNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYALPIKG 452 421 LIRCSSNITGLLTRDGGGENQTTEIFRPGGDMRDWRSELYKYKVVKIEBLGVAPTKA 480 11	YEAUTY 2 V POLYPROTEIN precursor - human immunodeficiency virus type 1 (strain YU-2) V POLYPROTEIN DECURSOR - human immunodeficiency virus type 1 (strain YU-2) Contains: coat protein gp190; coat protein gp41 Contains: coat protein gp190; coat protein gp41 Bacte: how human immunodeficiency virus type 1; HIV-1 Date: host Homo appiens (man) Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004 Molecule (man) Li. Y: Hui, H:, Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M. Li. Y.; Hui, H:, Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M. Title: Complete nucleotide sequence, genome organization, and biological properties of Reference number: A44001; MUID: 93021387; PMID: 1404605 Reference number: A44001; MUID: 93021387; PMID: 1404605 Reference number: A44001; MUID: 93021387; PMID: 1404605 References underer: A44001; MUID: 93021387; PMID: 1404605 Residues: 1-843 *cliv. Cross-references: UNIPROT: P35961; UNIPARC: UPIO00012A026; GB: M93258 Genetics: G	0

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A,Residues: 1-852 <MCC>
A,Cross-references: UNIPROT:O41883; UNIPARC:UPI000010B1F2; EMBL:U90934; NID:92351783; PI
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             3 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF
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                                                    RCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR
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81.7%; Score 2837; DB 2;
Best Local Similarity 83.1%; Pred. No. 3.7e-200;
Matches 541; Conservative 35; Mismatches 53;
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A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
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C; Species: human immunodeficiency virus type 1, HIV-1
C; Species: human immunodeficiency him 16-Jul-1999 #text_change 09-Jul-2004
C; R; Pang, (S; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, Bubminhated to the EMBL Data Library, July 1996
A; Reference number: Z16673
A; Reference number: Z16673
A; Reference number: L944
A; Residues: prelliminary; translated from GB/EMBL/DDBJ
A; Residues: Jr847 cpan>
A; Residues: Jr847 cpan>
A; Residues: L847 cpan>
A; Residues: L847 cpan>
A; Cosserreferences: UNIPROT: Q75760; UNIPARC: UP1000010C516; EMBL: U63632; NID: g1465777; Pl
A; Genetics:
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A; Cspecifamily: type E retrovirus env polyprotein
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                                                                                            KAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLRA 538
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LNGSLABEEIVIRSENFTDNAKTIIVHLNESVEINCTRPNNNVRRRHIHIGPGRAFY-TG
                                                                                                                                 KGLIRCSSNITGLLLTRDGGGENQTTRIPRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT
                           EILGNIRQAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGE
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82.8%; Pred. No. 4.4e-201;
ive 40; Mismatches 52; Indels
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536; Conservative
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Dandekar, S virus (HIV-3

OY 543 QHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKTLDQI 602	nan immunodeficiency virus type 1, HIV-1 Jomo sapiens (man)	Query Match Query Match B1.1*; Score 2816.5; BB 1; Length 852; Batches 528; Conservative 53; Mismatches 43; Indels 31; Gaps 7; Qy 3 LWVIVYYGVDVWKEATTILFCASDAKAYDTEAHNVMATHACVPTNPNPQEVVLENVTENF 62	QY 63 NAWKONIAVEQWHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTINTTELSIIVVWEQ 122	QY 179 UITQACPKUSPEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQL 238 DD 200 UITQACPKVTFBPIPIHYCAPAGFALLKCNNKKFNGTGPCTNVSTVQCTHGIRPVVSTQL 259 QY 239 LLNGSLAEBEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTG 298 DD 260 LLNGSLAEBEVVIRSENFTNNVKTIIVQLNVSVEINCTRPNNHTRKRTTWGPGRVYYTTG 319	OY 299 ELIGNIRQAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVWHSFNCGGE 358	OY 417 PIKGLIRCSSNITGLLITRDGGENGTTEIFRPGGEDMRDNWRSELYKYKVYKIEFLG 474
Db 436 RGQIRCSSNITGILITRDGGTNNSTNETFRPGGGDMRDNWRSELYKKVVKIEDLGVAPT 495 Qy 479 KAKREVVQREKRAVGALGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLRA 538	RESULT 6 S132BJ env protein - human immunodeficiency virus type 1 C;Species: human immunodeficiency virus type 1, C;Species: human-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 C;Schccesion: S132B9 A;Reference number: S132B9 A;Reference number: S132B9 A;Reference number: S132B9 A;Reference humany A;Molecule type: DNA A;Residues: 1-847 coBR> A;Residues: 1-847 coBR> A;Residues: 1-847 coBR> A;Residues: humany A;Re	Cysuperramity: type E fectovirus env polyprocein Query Match B1.6*; Score 2836.5; DB 2; Length 847; Best Local Similarity 82.5*; Pred. No. 4e-200; Matches 534; Conservative 39; Mismatches 55; Indels 19; Gaps 4; Qy 3 LWYLVYGVPVWKEATTILECASDARAYDTEAHNVWATHACVPTNPNPORVVLENVTENF 62	ACVPTDPNPQEVVL DLNTNNTTNTTELS : : DVNATNTTNDSEGT KNTTNNTKYRLINC	TSVITQ QLLLNG QLLLNG TGEILG	Db 261 SLAEBEVVIRSDNFTNNAKTIIVQLKESVEINCTRPNNNTRKSIHIGPGRAFYTTGEIIG 320 Qy 303 NIRQAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNOSSGGDPEIVMHSFNCGGFFYC 362 1	Db 381 NSTQLNNSTWNNNTEGSNNTEGNITIECRIKQFINMQEVGRAMYAPPIRGQI 434 Qy 423 RCSSNITGLLITRDGGGENQTTEIFRPGGDMRDNWRSELYKYKVKYKIEPLGVAPTKAKR 482

Db 551 LLMAIEAQQHMLELTVWGIKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASW 610 Qy 595 SNKTLDQIWNNMTWNEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQLDKWASL 649	540 KAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPW
NEBSULT 8 VCLLAA2 NALetrate names: coat polyprotein Cidypecies: human immunodeficiency virus type 1 (isolate ARV-2) NiAlternate names: coat polyprotein Cidypecies: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004 C;Accession: A03976 C;Accession: A03976 A;Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sh Science 227, 484-492, 1985 A;Title: Nuclectide sequence and expression of an AIDS-associated retrovirus (ARV-2). A;Reference number: A04003; MUID:85090453; PMID:2578227 A;Recession: A03976 A;Molecule type: DWA A;Residues: 1-855 <san> A;Residues: 1-855 <san> C;Genetics:</san></san>	RESULT 9 S13288 env protein - human immunodeficiency virus type 1 C; pate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004 A; Pitle: HIV-1 tropism for monounclear phagocytes can be determined by regions of gpl20 A; Pate number: S13288 MUID: 91043044; PMID: 2172833 A; Accession: S13288 A; Retaus: preliminary A; Molecule type: DMA A; Residues: 1-854 *COBR> A; Residues: 1-854 *COBR> A; Cross-references: UNIPROT: Q72502; UNIPROT: 090178; UNIPROT: Q78243; UNIE
Ajouer: ean; type E retrovirus env polyprotein C; Superfamily: type E retrovirus env polyprotein; Glycoprotein; immunodeficiency; polyprot C; Superfamily: and and protein; coat protein; glycoprotein; immunodeficiency; polyprot F;1-30/Domain: signal sequence #status predicted <sig>F;31-509/Product: exterior membrane glycoprotein #status predicted <ext>F;310-855/Product: transmembrane glycoprotein #status predicted <tmm>F;87,129,140,158,184,190,200,244,265,298,304,334,341,358,364,388,394,400,408,445,458</tmm></ext></sig>	Query Match 80.9%; Score 2809.5; DB 2; Length 854; Best Local Similarity 82.8%; Pred. No. 3.8e-198; Matches 539; Conservative 34; Mismatches 57; Indels 21; Gaps 9; Qy 3 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPOEVVLENVTENF 62 Db 34 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLVNVTENF 93
Ouery Match 81.0%; Score 2815.5; DB 1; Length 855; Best Local Similarity 81.2%; Pred. No. 1.4e-198; Matches 528; Conservative 47; Mismatches 58; Indels 17; Gaps 6;	QY 63 NWWKNNWVEQWHEDIISLWDGSLKPCVKLTPLCVTLNCTDLNTNNTTELSIIVVWEQ 122
Oy 3 LWVTVYSGVPVWKGATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPOEVVLENVTENF 62 	QY 123 RGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSVITQ 182 ::
Qy 63 NAWKNINWEQWHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNTTELSIIVVWEQ 122	QY 183 ACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG 242
Qy 123 RGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEBIDDNKVTTNNTKYRLINCNTSVITQ 182 ::	OY 243 SLAEEEVVIRSENFTNNAKTIIVQLANVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEI 300 :
OY 183 ACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGFCTNVSTVQCTHGIRPVVSTQLLLNG 242	QY 301 LGNIRQAHCNISRAQMNNTLQQIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEF 359 :
Qy 243 SLABEBEVURSENFTNNAKTIIVQLAVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEILG 302 	QY 360 FYCHSTOLFNSAMNVTSNGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYALPI 418
QY 303 NIRQAHCNISRAQWINTLQQIATTLREQFG-NKTIAFNQSSGGDBEIVWHSFNCGGEFFY 361.	QY 419 KGLIRCSSNITGLLLTRDGGGBNQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT 478
Oy 362 CNSTQLFNSAWNVT-SNGFWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYALPIKG 420	OY 479 KAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQNNLLRA 538
OY 421 LIRCSSNITGLLTRDGG-GENQTTEIFRPCGGDWRDNWRSELYKKKVVKIEPLGVAPTK 479	QY 539 IKAQOHLLQLTVWGIKQLQARILAVBRYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKT 598 -
QY 480 AKRRVVQREKRAVGMLGAMFLGFLGAAGSTWGATSWALTVQARQLLSGIVQQQNNLLRAI 539	Oy 599 LDQIMNNMTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQLDKWASL 649 :

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C.Superfamily: type E retrovirus env polyprotein
C.Keywords: coat protein; glycoprotein; polyprotein, transmembrane protein
C.Keywords: coat protein; glycoprotein; polyprotein, transmembrane protein
F;1-699/bomain: extracellular #status predicted <EXT>
F;1-33/Region: hydrophobic #status predicted <SIG>
F;17-33/Region: hydrophobic #status predicted <CPI>
F;14-517/Region: coat protein gp10 #status predicted <CPI>
F;514-517/Region: cleavage processing #status predicted <CPI>
F;518-617/Region: hydrophobic #status predicted <CPI>
F;518-617/Region: hydrophobic #status predicted <TMI>
F;712-861/Domain: intracellular #status predicted <IMI>
F;712-861/Domain: intracellular #status predicted <IMI>
F;712-861/Domain: hydrophobic #status predicted <IMI
F;712-861/Domain: hydrophobic #status hydr
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R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated A;Reference number: A42995; MUID:92351552; PMID:1322587
                                                                                                                                                                                                                                                                                                                                                                                                                                                     env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)
N/Alternate names: coat polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-861 <SHI>
A;Cross-references: UNIPROT:P31819; UNIPARC:UP1000012A019; GB:S41266; GB:D01206
    596
                                              151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Note: host Homo sapiens (man)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                                       597 KTLDQIWNNMTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQLDKWASL
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C;Species: human immunodeficiency virus type 1, HIV-1
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80.8%; Score 2808; DB 1;
Best Local Similarity 81.8%; Pred. No. 5e-198;
Matches 534; Conservative 49; Mismatches 48
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F;690-711/Domain: transmembrane #status predicted <TM1>
F;712-729/Domain: intracellular #status predicted <INT>
F;93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414
                                                                                                 MyAlternate names: cost polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)
NyAlternate names: cost polyprotein
NyAlternate names: cost protein gp120;
Cspecies: human immunodeficiency virus type 1, HIV-1
A;Note: host Home sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
C;Accession: B42995
R;Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
N;Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated A;Reference number: A42995; MUID:92351552; PMID:1322587
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C;Genetics:
A;Gene: env
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80.8%; Score 2808; DB 1
Best Local Similarity 81.8%; Pred. No. 4e-198;
Matches 534; Conservative 49; Mismatches 4
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A; Residues: 1-729 <SHI>
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422 IRCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVA 476		RAIKAQOHLLQLIVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPMNASWSN	KTLDQIWNNWTWAWBEDDNYTHLIYTLIEESQNQOEKNQOELLQLDKWASL 649 : : : -	. 12	VCLUH3 WILDH3 WINDH3 WAlternate names: coat polyprotein C.Species: human immunodeficiency virus type 1 (isolate HTLV) WALTERNATE NAMES: COAT POLYPROTEIN C.Species: human immunodeficiency virus type 1, HIV-1	on 17-May-1985 #text_change 09- . R.; Livak, K.J.; Starcich, B.	allo, R.C.; wc , HTLV-III.	prence number: A93353; MUID:85111123; PMID:2578615 sssion: A03973 ecule type: DNA	.cues: 1-856 crat.> ss-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K0200 s. env	rfamily: type E retrovirus env polyprotein ords: 1105; capsid protein; alycoprotein; immunodeficiency	F;1-5)-Comarm: signal sequence meratus predicted v315 F;31-511/Product: exterior membrane glycoprotein #status predicted <ext> F;512-856/Product: transmembrane glycoprotein #status predicted <tmm> F;812-85.441,156,160,1332,1332,339,356,381 F;611.616,625,637,678,816/Binding site: carbohydrate (Asn) (covalent) #stat</tmm></ext>	Length 856;	'miniming' oz.3*, fred. NO.; ; Conservative 35; Mismatc LWVTVYYGVPVWKEATTTLFCASDAKAYDT		6.3 NOWAKUWA KAMBADI SEMDOSEKECYKLIPICYILAYOTDLAYINYITHTEESII IVVWEQ 12.2 9.4 NOWAKUDWVEQMHEDIISEMDOSEKECYKLIPICVEKKCIDLKUDININSSSGRMIME- 15.0	123 RGKGEMENCSFNITTSIRDKVQREYALPYKLDVEPIDDNKNTTNNTKYRLINCNTSVITQ 182		183 ACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG 242	243 SLABEBEVVIRSENFTNNAKTIIVQLAVSVEINCTRENNHTRKRVTLGEGRVWYTTGEI 300		SOT DONING PHICKLES AND LOCATED THE BOLD OF THE WOOSE COLDER VINES FINCES SON

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ALIGNMENTS

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Total number of hits satisfying chosen parameters:

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2166443 seqs, 705528306 residues

Gapop 10.0 , Gapext 0.5

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Scoring table:

Searched:

1 ANLWVTVYYGVPVWKEATTT.....QNQQEKNQQELLQLDKWASL

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MEDLINE=90253924; PubMed=2187500;
Kalyanaraman V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,
DeVico A.L., Copeland T., Oroszlan S., Gallo R.C., Sarngadharan M.G.;
"Characterization of the secreted, native gp120 and gp160 of the human Human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1). Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group. 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)]. MEDLINE=87041461; PubMed=3490666;
Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
Andersen P.R., Pevare S.G.;
"Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant AIDS; Capsid protein; Direct protein sequencing; Glycoprotein; Polyprotein; Signal; Structural protein; Transmembrane. divergence in its genomic sequences."; Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986) HSSP, P19549; IMEQ. SMR; P05679; 84-128, 87-212, 206-503, 552-638. HIV; MI3137; ENV\$CDC45. INCEPEPO; IPRO00328; ENV GP41. InterPro; IPRO00777; GP120. immunodeficiency virus type 1."; AIDS Res. Hum. Retroviruses 6:371-380(1990). 868 AA EMBL; M13137; AAA44311.1; -; Genomic_RNA. PIR; C25523; VCLJH4. PRT; Pfam; PF00516; GP120; 1. Pfam; PF00517; GP41; 1. STANDARD; NUCLEOTIDE SEQUENCE NCBI_TaxID=11687; ENV HV1C4 P05879; Name=ENV; removed. ENV_HV1C4

Ared. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Minimum Match 0% Maximum Match 100% Listing first 45 summaries UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* length: 0 length: 2000000000 Post-processing:

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& Query Match		100.0	84.3	83.7	83.7	83.6	83.5	83.4	83.4	83.4	83.4	3	83.3	83.3	83.2	ë.		83.2	83.2	83.1	83.1	83.1	83.1	83.1	83.1	83.1	83.0	83.0	83.0	83.0	83.0	83.0
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Exterior membrane glycoprotein.
Transmembrane glycoprotein.
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).

33 522 868 89 131

Polyprotein; SIGNAL CHAIN 3 CHAIN 52 CARBOHYD 6 CARBOHYD 13

523 89 131

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NEDLINE=22628496; PubMed=12743293;

NEDLINE=22628496; PubMed=12743293;

NOI=10.1128/JVI.77.11.6359-6366.2003;

Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.,

Brown T.W., Salemi W., Vandamme A.M., Kalish M.L.;

I.S. Human immunodeficiency virus type 1 epidemic: date of origin,

population history, and characterization of early strains.";

J. Virol. 77:6359-636(2004)

BRBL; AY247222; AAP37150.1; -; Genomic_DNA.

RSSP, P04578; 1DDB.

RNR; O78VL3; 2-154, 195-489, 538-624.

GO; GO:0019031; C:integral to membrane; IEA.

GO; GO:0019031; C:integral molecule activity; IEA.

InterPro; IPR000328; Env GP41.

InterPro; IPR00077; GP120.

R Pfam; PP00517; GP120; 1.
     93 NWWKNNWVEQMHEDIISLWDGSLKPCVKLTPLCVTLNCT--NLRNTTNTTSSS----WGT
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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
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85.5%; Pred. No. 2.8e-223;
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ID Q7SVL3 9HIV1 PRELIMINARY;
AC Q7SVL3;
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BMBL, AN357520; AR00883.1; -; Genomic_DNA.
HSSP: P04578; IK33.
SMR; QGUYR2; 196-493, 541-627.
 NLWVTVYYGVPVWKBATTTLFCASDAKAYDTBAHNVWATHACVPTNPNPQEVVLENVTEN
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Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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05-JUL-2004 (TrEMBLrel. 27, Last ann
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QGUYR2;
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Theodore T.S., Englund G., Buckler-White A., Buckler C.E.,
Martin M.A., Peden K.W.;
"Construction and characterization of a stable full-length macrophage-
tropic HIV type 1 molecular clone that directs the production of high
titers of progeny virions.";
AIDS Res. Hum. Retroviruses 12:191-194(1996).
                                                IRÇSSNITGLLITRDGGKDENGTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKA
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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae, Lentivirus, Primate lentivirus group.
VGBI_TaxID=11676;
SLAEBEVVIRSDNFTDNAKTIIVQLNESVEINCTRPNNNTRKSINIGPGRAFYATGEIIG
                                 NIROAHCNISRAQWNNTLOQIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEFFY
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Martin M.A., Peden K.W.C.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AP004334; AAB64170.1; -; Genomic_DNA.
HSSP; P04578; 1DLB.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:integral to membrane; IEA.
InterPro; IPR000328; Env GP91.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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84.0%; Pred. No. 9.1e-222;
ive 36; Mismatches 48;
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CE 854 AA; 97291 MW; 06
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Best Local Similarity 84.0
Matches 548; Conservative
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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                                                                                                                                               Length 853;
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                                                                                                                                         83.7%; Score 2906.5; DB 2;
83.7%; Pred. No. 1.2e-221;
ive 46; Mismatches 47;
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MEDLINE=22628496; PubMed=12743293;
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
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Q7SVL7;
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Matches 543; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWEQ 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 MEKGEIKNCSFNITTNIRDKMQKEYALFYRLDVVPID---NDSTNTSYRLISCNTSVITQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 DIRQAHCHLSRTKWANTLRQIVYKLREQFGNKTIVFNQSSGGDPEIVTHSFNCGGEFFYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 ACPKVSFEPIPIHYCTPAGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVISTQLLLNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLIRCSSNITGLLLTRDGG-GENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEFLGVAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 GQIRCSSNITGLLLTRDGGNNKSETTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLLRA
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A Robbins K.B., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S. A Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;
T. "U.S. Human immunodefficiency virus type 1 epidemic: date of origin population history, and characterization of early strains.";
J. Virol. 77:6359-6366(2003).
R RBL; AY247218; AAP37146.1; -; Genomic_DNA.
R RSSP; P20871; 1CE4.
R SMR; Q7SUL7; 195-496, 541-630.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0016031; C:integral to membrane; IEA.
R GO; GO:0019031; C:viral envelope; IEA.
R GO; GO:0019031; C:viral envelope; IEA.
R InterPro; IPR000328; Enructural molecule activity; IEA.
R InterPro; IPR00077; GP120.
R Pfam; PF00516; GP120; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.6%; Score 2905; DB 2;
84.2%; Pred. No. 1.6e-221;
                                                                                                                                                                                                                                                                                                                                                                                                         Envelope protein; Transmembrane.
NCE 860 AA; 97762 MW; A7E185F2BD421590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
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QGUYPO;
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 84.2
Matches 548; Conservative
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63 NAWKONNWVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWEQ 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             572 RAIEAQQHLLQLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKIICTTAVPWNASWSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 VITQACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1.
Viruses, Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FFYCNSTOLFNSTWNASS - - TWNDTEGSNNTEGTITLPCRIKQIINMWQEVGKAMYAPPI
                                                                                                                                                                                                                                                                                                                                                                                                        origin,
                                                                                                                                                                                                                                                                                                         (1)
WCLEOTIDES SEQUENCE.
MEDLINE=2262846; PubMed=12743293;
DOI=10.1128/JV1.77.11.6359-6366.2003;
Mobbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S., Brown T.M., Salleni M., Vandamme A.M., Kallsh M.L.;
Brown T.M., Salleni M., Vandamme A.M., Kallsh M.L.;
"U.S. Human immunodeficiency virus type 1 epidemic: date of orig: population history, and characterization of early strains.";
"J. Virol. 77:6359-6366(2003).
EMBL; AY247220; AAP37148.1; -; Genomic_DNA.
                                                  22;
                                 597 KTLDQIWNNMTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQLDKWASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.4%; Score 2899; DB 2; Length 852; 83.9%; Pred. No. 4.7e-221; ive 36; Mismatches 47; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  952 AA; 96680 MW; F8D811028025D998 CRC64;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA
GO; GO:0005198; F:structural molecule activity; IEA
                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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                                                                                                                                          852
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InterPro; IPR000777; GP120.
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                                                                                                                                        Q7SVL5_9HIV1 PRELIMINARY;
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Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                    Envelope glycoprotein.
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Matches 546;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMeda-1499699; DOI=10.1128/JVI.78.6.2790-2807.2004; Fulbmeda-1499699; DOI=10.1128/JVI.78.6.2790-2807.2004; Kuhmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L., Sinyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A., Korber B.T., Wolinsky S.M., Moore J.P.; "Genetic and phenotypic analyses of human immunodeficiency virus type 1 escape from a small-molecule CCR5 inhibitor."; J. 18:2790-2807(2004).

EMBL: AY357551; AAR00905.1; -; Genomic_DNA.
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                                                                         Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                         SMR; Q6UYP0; 93-147, 209-507, 552-641.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR000328; Env GP41.
(TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.5%; Score 2900.5; DB 2;
83.5%; Pred. No. 3.6e-221;
ive 45; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                   AIDS; Envelope protein; Transmembrane.
                                 Envelope glycoprotein (Fragment).
                                                            Human immunodeficiency virus 1.
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Matches 545; Conservative
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Pfam; PF00517; GP41; 1.
                                                                                                                                     NUCLEOTIDE SEQUENCE
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SEQUENCE
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01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Surface envelope glycoprotein.
Surface envelope glycoprotein.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
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MEDLINE=91195299; PubMed=2014229;

Westervell F., Gendelman H.E., Ratner L.;

Westervell F., Gendelman H.E., Ratner L.;

Widentification of adeterminant within the human immunodeficiency virus 1 surface envelope glycoprotein critical for productive infection of primary monocytes.";

FORC. Natl. Acad. Sci. U.S.A. 88:3097-3101(1991).

EMBL; MG0472; AAA45065.1; -; Genomic_RNA.

MSSP; P20871; 1C84.

SMR; Q03811; 143-488, 537-623.
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity;
InterPro; IPR000328; Env GP41.
InterPro; IPR00777; GP120.
Pfam; PF00516; GP120; 1.
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83.6%; Pred. No. 7.4e-221;
ive 40; Mismatches 48;
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SEQUENCE 853 AA; 96998 MW; AD2AF21
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W. Kuhmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
A Snyder A., Strizki J.W., Riley J., Baroudy B.M., Wilson I.A.,
A Snyder A., Strizki J.W., Moore J.P.;
Wolinsky S.M., Moore J.P.;
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Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae,
Lentivirus, Primate lentivirus group.
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82.5%; Pred. No. 5.3e-221;
.ive 48; Mismatches 50; Indels
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
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                        --GMRGEIKNCSFNITTSIRDKVKKDYALFYRLDVVPIDN----DNTSYRLINCNTSTI
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
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EMBL; AX357554; AAR0908.1; -; Genomic_DNA.
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SMR; Q6UXN7; 93-147, 209-507, 555-641.

G0; G0:0016021; C:integral to membrane; IEA.

G0; G0:0019031; C:viral envelope; IEA.

G0; G0:0005198; F:structural molecule activity; IEA.

InterPro; IPR000128; Env GP41.

InterPro; IPR000177; G9120.

Pfam; PF00517; GP120; 1.
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QGUNN';
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
VCBI_TaxID=11676;
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DOI=10.1128/JVI.77.11.6359-6366.2003;
Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.
Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;
"U.S. Human immunodeficiency virus type 1 epidemic: date of orig."
"Pupulation history, and characterization of early strains.";
Virol. 77:6599-6366(2003).
                                           19;
  Length 863;
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Score 2896.5; DB : Pred. No. 7.6e-221 45; Mismatches 48
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EMBL; AY247221; AAP37149.1; -; Genomic_DNA.
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Q7SVL4;
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Best Local Similarity 83.1.
Matches 544; Conservative
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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                                                                                                                                                                                                                                                                  43; Indels
                                                                                                                                                                                        62ED5F6AB033D20B CRC64;
HSSP; P20871; 1CE4.
SMR; Q78VL4; 195-486, 534-620.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0001998; Fstructural molecule activity; IEA.
InterPro; IPR000328; Env GP41.
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Last annotation update)
                                                                                                                                                                                                                           b; Score 2895; DB 2;
b; Pred. No. 9.7e-221;
33; Mismatches 43;
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                                                                                                                            Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Envelope protein; Transmembrane.
SEQUENCE 850 AA; 96583 MW; 62ED5F
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Q7SUV4;
01-OCT-2003 (TEMBLEEL 25, C.
01-OCT-2003 (TEMBLEEL 25, L.
01-MAR-2004 (TEMBLEEL 26, L.
Envelope glycoprotein.
                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.9%;
Matches 552; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 FINAMKNINAVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 GSLAEEEVVIRSENFTWAKTIIVQLNETVEINCIRPNNNTRKGIHIGPGRTFYTTGDII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 YCNSTQLFNSAWNVTSNGTW----SVTRKQKDTGDIJTLPCRIKQIINRWQVVGKAMYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       861;
NUCLEOTIDE SEQUENCE.
MEDIINE=22533916; PubMed=12646921; DOI=10.1038/nature01470; Wei X., Decker J.M., Wang S., Hui H., Kappes J.C., Wu X., Salazar-Gonzalez J.F., Salazar M.G., Kilby J.M., Saag M.S., Komarova N.L., Nwak M.A., Hahn B.H., Kwong P.D., Shaw G.M.; "Antibody neutralization and escape by HIV-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                             Nature 422:307-312(2003).

Nature 422:307-312(2003).

RNBL; AY22324, AAP57324.1; -; Genomic_RNA.

HSSP; P04578; 1DLB.

SMR; QOSON 545-61.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:virtal envelope; IEA.

GO; GO:0019031; C:virtal envelope; IEA.

InterPro; IPR000328; Env GP41.

InterPro; IPR000377; GP120.

Pfam; PF00517; GP120, 1.

Pfam; PF00517; GP121; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          AIDS; Envelope protein; Transmembrane.
SEQUENCE 861 AA; 98313 MW; 4E8A3F4278A9E302 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.3%; Score 2893.5; DB 2
83.1%; Pred. No. 1.3e-220;
ive 42; Mismatches 50;
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NMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDL-NTNNT--TNTTELSIIVV 119
                       380 FYCNSTQLFNSTW-------KDTGELMNPEGNSNITLPCKIKQIINRWGGVGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 ITQACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLL
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                                                                                                                                                   AMYALPIKGLIRCSSNITGLLLTRDGGGE-NQTTEIFRPGGGDMRDNWRSELYKYKVVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                Envelope glycoprotein.
Human immunodeficienty virus 1.
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Geels M.J., Jansen C., Baan E., De Cuyper I.M., van Schijndel G.J.N. Pollakis G., Schuitemaker H., Bakker M., Goudsmit J., van Baarle D. Baxton W.A., Miedema F.;

"Differential loss of human immunodeficiency virus type I (HIV-1) - specific T-helper responses in two HIV-1 infected individuals following CTL escape.";

Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; AY970947; AAX86729.1; -; Genomic DNA.

GO, GO:0019031; C:viral envelope; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIDS; Envelope protein; Transmembrane.
SEQUENCE 851 AA; 96407 MW; A447E60789932CF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.2%; Score 2890.5; DB 2; 83.5%; Pred. No. 2.2e-220; ive 35; Mismatches 35;
                                                                                                                                                                                                                                                                                                       851
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                                                                                                                                                                                                                                                                                                       9HIV1 PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                       PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004; Kuhmann S.E., Pupach P., Kunstmann K.J., Taylor J., Stanfield R.L., Kuhmann S.E., Pupach P., Kunstmann K.J., Taylor J., Stanfield R.L., Snyder A., Strizki J.M., Rilley J., Baroudy B.M., Wilson I.A., Korber B.T., Wolinsky S.M., Moore J.P.; "Genetic and phenotypic analyses of human immunodeficiency virus type I escape from a small-molecule CCRS inhibitor."; J. Virol. 78:2790-2807(2004).
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
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83.1%; Pred. No. 1.6e-220;
ive 44; Mismatches 52; Indels
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GG:0016021, Cintegral to membrane; IEA.
GG:0019031, C:viral envelope; IEA.
GO:0005198; F:structural molecule activity; IEA.
                                                                    (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
867 AA
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                                                  Created)
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InterPro; IPR000777; GP120.
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PRELIMINARY;
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T. "Genetic and phenotypic analyses of human immunodeficiency virus type I escape from a small-undecule CCRS inhibitor.";

J. Virol. 78:2790-2807(2004).

R. EMBL, AN357555, AAR00909.1; -; Genomic_DNA.

SNR, GGVING; 93-147, 557-643.

R. GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0015031; C:viral envelope; IEA.

GO; GO:005198; P:structural molecule activity; IEA.

R. InterPro; IPR000328; Env GP41.
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Envelope glycoprotein (Fragment).
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83.0%; Pred. No. 2.7e-220;
iive 46; Mismatches 52;
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Pfam; PF00517; GP41; 1.
AIDS; Envelope protein; Transmembrane.
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83.3%; Pred. No. 1.5e-229;
ive 40; Mismatches 38; I
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APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
US-08-463-209-11
US-09-337-387-11
US-08-127-499A-14
US-08-472-240A-1
US-08-472-240A-1
US-08-472-240A-1
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US-07-956-483-13
US-08-448-603A-32
US-09-492-739-32
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; Sequence 2, Application US/09476242
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; GENERAL INFORMATION:
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APPLICANT: Berman, Phillip W.
APPLICANT: Nadamura, Gerald R.
TITLE OF INVENTION: HIV Envelope Polypeptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
STREET: 3 Embarcadero Center
CITY: San Francisco
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APPLICATION NUMBER: US/09/134,075
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NAME: Haliday, Emily
REGISTRATION NUMBER: 38903
REFERENCE/DOCKET NUMBER: 14918-704
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2000
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APPLICATION NUMBER: 08/448,603
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382 NSTQLFNSTWNNTIGPNNTNGT------ITLPCRIKQIINRWQEVGKAMYAPP 428
                                                                                                                                                                                                               NMWKONNWUEQWHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWEQ 122
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                                                                                                                                                                                           RAIKAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSN
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83.0%; Pred. No. 6.2e-227;
ive 42; Mismatches 52; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP STREET: 3 Embarcadero Center CITY: San Francisco CITY: CA Francisco COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOCTWARE: FASECEMO FOR WINDOWS Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/448,603A
FILING DATE: 07-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/072,833
FILING DATE: 07-JUN-93
ATTORNEY/AGENT INFORMATION:
NAME: HALIGAY, EMILY
REGISTRATION NUMBER: 38903
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
APPLICANT: Nakamura, Gerald R.
TITLE OF INVENTION: HIV Envelope Polypeptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14918-704
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Patent No. 5864027
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2286
TELEFAX: 415-393-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 850 amino acids
TYPE: amino acid
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Best Local Similarity 83.0
Matches 537; Conservative
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                                                                                                                                                    NAWKONIMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWEQ
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                                                                                                                                         LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF
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NUMBER OF SEQUENCES: 33
CORESPONDESSE: ADDRESS:
ADDRESSE: McCutchen, Doyle, Brown & Enersen, LLP
STREET: 3 Embarcadero Center
CITY: San Francisco
STATE: CA
                                                                                                                      Indels
                                                                                                                      52;
                                                                                                  82.1%; Score 2852; DB 2; 83.0%; Pred. No. 6.2e-227; ive 42; Mismatches 52;
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                    28:
                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 850 amino acids TYPE: amino acid
                                                                                                Query Match
Best Local Similarity 83.0
Matches 537; Conservative
415-393-2286
                                                           single
                                                                   linear
                                                          STRANDEDNESS:
                                                                   COPOLOGY:
                                                                              US-09-134-075-28
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US-09-492-739-28
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                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/492,739
FILING DATE: 27-Jan-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2852; DB 2;
Pred. No. 6.2e-227;
42; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 14918-704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/134,075
                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Haliday, Emily
REGISTRATION NUMBER: 38903
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 850 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 415-393-2000
                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-393-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 83.0%;
Matches 537; Conservative 42
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
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INFORMATION FOR SEQ ID NO:
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262 SLAEBEVVIRSANFSDNAKTIIVQLNESVEINCTRPNNNTRRSIHIGPGRAFYATGEIIG 321
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                                                                                                                                                                                                381 NTTPLFNSTWNYTY -- TWNNTEGSNDTGRNITLQCRIKQIINMWQEVGKAMYAPPIRGQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Franchini, Genoveffa
APPLICANT: Markham, Phillip D.
APPLICANT: Gallo, Robert C.
APPLICANT: Lori, Franco C.
APPLICANT: Popovic, Mikulas
APPLICANT: Garner, Suzanne
ITILE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
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ZONIATER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUDRESSEB: CUSHMAN, DARBY & CUSHMAN STREET: Bleventh Floor, 1615 L. Street, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/599,491
FILING DATE: 17-0CT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/70
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08022835 Patent No. 5420030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reitz Jr., Marvin S. APPLICANT: Franchini, Genoveffa
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INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
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JS-08-022-835-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 ACPKVSFEPIPIHYCAPAGFAILKCRDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG 261
557 QHLLQLTVWGIKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSNKSLDKI 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 SLAEEBVVIRSENFINNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEILG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 LWUTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVFTDPNPQEIGLENVTENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG
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                                                                Length 850;
                                                                                                                                                                                                                                                                                                                                                                                  Brown & Enersen, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                          Nakamura, Gerald R.
TITLE OF INVENTION: HIV Envelope Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.1%; Score 2852; DB 2;
83.0%; Pred. No. 6.2e-227;
tive 42; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/966,931A
FILING DATE: 27-Sep-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 14918-704
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-966-931A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/492,739
                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: McCutchen, Doyle,
STREET: 3 Embarcadero Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: <Unknown>
ATTORNEY/AGENT INFORWATION:
NAME: Haliday, Emily
REGISTRATION UNMERE: 38903
                                                                                                                                                                                             Sequence 28, Application US/09966931A Patent No. 6806055 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 850 amino acids
                                                                                                                                                                                                                                                                   APPLICANT: Berman, Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-393-2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 83.0 Matches 537; Conservative
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                           US-09-966-931A-28
                                            603
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,835
FILING DATE: 2-FEB-1937
APPLICATION NUMBER: US 07/599,491
FILING DATE: 17-0CT-1990
ATTONEY/AGENT INFORMATION:
NAME: LESLIE A. SERUNIAN
REGISTRATION NUMBER: 35,353
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                MEDIUM TYPE: FLOPPY DISK, 3.5"
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,809
FILING DATE: 15-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-388-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                  120 WEQRGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 GQIRCSSNITGLILITRDGGPEDNKTEVFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTK 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 FYCNSTQLFNSTWNVTEESNNTV-----ENNTITLPCRIKQIINMWQEVGRAMYAPPIR 438
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                                                                                                                                                                                                 33 LWVTVYYGVPVWKEATTTLFCASDRKAYDTEVHNVWATHACVPTDPNPOEVELKNVTENF
                                                                                                                                                                                                                                                                              93 NIWWKNINWVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLRNATNGNDTNTTSSSRGWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 LNGSLAEEEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGE
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                                                                                              81.6%; Score 2834; DB 1; Length 855; 82.2%; Pred. No. 1.9e-225; ive 45; Mismatches 53; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   618 NXIWDNWTWIEWDREINNYTSIIYSLIEESQNQQEKNEQELLELDKWASL
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Patent No. 5576000
GENERAL INFORMATION:
APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,
APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND
APPLICANT: GARTNER, SUZANNE
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                            Query Match 81.6
Best Local Similarity 82.2
Matches 534; Conservative
                                      ; MOLECULE TYPE: protein US-08-022-835-6
amino acid
GY: linear
                      TOPOLOGY:
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(212) 751-6849

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                                                                                                                                                                                       NAWKNINAVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLRNATNGNDTNTTSSSRGMV 152
                                                                                                                                                                                                                                              120 WEQRGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDWKNTTNNTKYRLINCNTSV 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 ITQACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLL
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                                                                                   3 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF
                                                                                                                                                                                                                                                                                                                                                  AKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKRRVVQREKRAVG-1GAVFLGFLGAAGSTMGAAAMTLTVQARLLLSG1VQQQNNLLRA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKTL
                                         18;
                                           53; Indels
; Score 2834; DB 1;
; Pred. No. 1.9e-225;
45; Mismatches 53;
  81.6%;
    Query Match
Best Local Similarity 82.24
Matches 534; Conservative
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ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK COUNTRY: USA

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240 INGSLAEEEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGE 299
                                                                   300 ILGNIRQAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNOSSGGDPEIVMHSFNCGGEF 359
                                                                                                                                                       360 FYCNSTQLFNSAWNVTSNGTWSVTRKQKDTGDIJTLPCRIKQIINRWQVVGKAMYALPIK 419
                                                                                                                                                                                                                                              385 FYCNSTQLFNSTWNVTEESNNTV----ENNTITLPCRIKQIINMWQEVGRAMYAPPIR 438
                                                                                                                                                                                                                                                                                                                                AKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLRAI 539
                                                                                                                                                                                                                                                                                                                                                                                                                                  557
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    105 ITQACPKVSFEPIPIHYCAPAGFAILKCKDKKFNGKGPCTNVSTVQCTHGIRPVVSTQLL 264
                                                                                                                                                                                                                                                                                                     GLIRCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTK 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKTL 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 NMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWEQ 122
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APPLICANT: SCHUELKE, NORBERT
APPLICANT: OLON, WILLIAM C
APPLICANT: OLON, WILLIAM C
APPLICANT: OLON, WILLIAM C
APPLICANT: JOHN, MOORE P
TITLE OF INVENTION: STABILIZED VIRAL ENVELOPE PROTEINS AND USES THEREOF
FILE REFERENCE: 2048/59331a
CURRENT APPLICATION NUMBER: US/09/602,864
CURRENT FILING DATE: 2000-06-23
FRIOR APPLICATION NUMBER: 60/141,168
FRIOR APPLICATION NUMBER: 60/141,168
FRIOR PEDICATION DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                               3 LWVIVYYGVPVWKEAITILFCASDAKAYDTEAHNVWAIHACVPINPNPQEVVLENVTENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLENVTEHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
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81.4%; Score 2827.5; DB 2; Length 643;
Best Local Similarity 82.2%; Pred. No. 4.5e-225;
Matches 532; Conservative 40; Mismatches 56; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOIWNNMTWMEWDREIDNYTHLIYTLIEESQNQOEKNQQELLQLDKWASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/09602864; Patent No. 6710173; GENERAL INFORMATION:
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Best Local Similarity
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 NWWKNNNYEQMHEDIISLMPQSLKPCVKLTFLCVTLNCTDLRNATNGNDTNTTSSSRGMV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITQACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLL 239
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                   18;
500 DQIWNNMTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQLDKWASL
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                                                                                                                                     Sequence 6, Application US/08647714

Patent No. 5869313

GENERAL INFORMATION:
APPLICANT: RETZ, JR., MARVIN S.; FRANCHINI,
APPLICANT: GENOVEFFA; MARKHAM, PHILIP D. GALLO, ROBERT
APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND
APPLICANT: C.; LORI, FRANCO
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZUPILITIE USA
ZUPILITIE READABLE FORM:
MEDIUM TYPE: FLOPPY DISK, 3.5"
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERRENCT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/388,809
FILING DATE: 15-PEB-1995
APPLICATION NUMBER: US 08/022,835
FILING DATE: 25-FEB-1993
APPLICATION NUMBER: US 07/599,491
FILING DATE: 17-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: LESLIE A. SERUNIAN
REGISTRATION NUMBER: 35,353
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       CITY: NEW YORK STATE: NEW YORK STATE: NEW YORK COUNTRY: USA
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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; STRANDEDNESS; single
TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-956-483-14
                                                                                           Best Local Similarity 81.39
Matches 534; Conservative
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MEDIUM TYPE: Floppy
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STRANDEDNESS:
TOPOLOGY: 11
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                                SLAEEEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEILG 302
                                                                                           NIRQAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGEFFYC 362
                                                                                                            NSTQLFNSAWNVTSNGTWSVTRKQKDTGDIJTLPCRIKQIINRWQVVGKAMYALPIKGLI 422
                                                                                                                                                                                     NSTOLFNSTWNNNTEGS-----NNTEGNTITLPCRIKQIINMWQEVGKAMYAPPIRGQI 405
                                                                                                                                                                                                                      RCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKR 482
                                                                                                                                                                                                                                                   RCSSNITGLLLTRDGGINENGTEIFRPGGGDMRDNWRSEFYKYKVVKIEPLGVAPTKCKR 465
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                                               ACPKISFEPIPIHYCAPAGFAILKCNDKTFNGKGPCKNVSTVQCTHGIRPVVSTQLLLNG
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                                                                                                                                                                                                                                                                                                                                                                                                                               SOLUBLE AND UNCLEAVED
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,483
FILING DATE: 31-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: KIENY, MATIE-PAULE
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AN
TITLE OF INVENTION: 9p.60 VARIANT
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
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APPLICATION NUMBER: W0 92/19742

FILING DATE: 12-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: F9 1 05392

FILING DATE: 02-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Crane-Feury, Sharon E

REGISTRATION NUMBER: 36,113

REFERENCE/DOCKET NUMBER: 017753-00

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/07956483
Patent No. 6261799
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGVAPTKAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQ 532
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                                                                                                                                                                                                          63 NWWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWEQ 122
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                                                                                                                                                                                                                                                                                                                                                 123 RGK---GEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSV
                                                                                                                                                                                                                                                                                                                                                                                                                     180 ITQACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 ILGNIRQAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPELVMHSFNCGGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 IIGDIRQAHCNISRAKMNYTLKQIVIKLRDQFENKTIIFNRSSGGDPELVMHSFNCGGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 FYCNSTÓLFSSTWNGTEGSNNTGG-----NDTITLPCRIKEIINWQEVGKAMYAPP
                                                                                                   3 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF
                                                                                                                               33 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNIWATHACVFTDPNPQEVVLGNVTENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 FYCNSTQLFNSAWNVT--SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 IKGLIRCSSNITGLLLTRDG-----GGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEP
                                                   Gaps
                                                   30;
DB 2; Length 855;
                                                   54; Indels
                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 4e-224; 39; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Sairo, Ateushi
APPLICANT: Sairo, Ateushi
APPLICANT: Sinagawa, Hideo
APPLICANT: Hakata, Ateuo
APPLICANT: Hakata, Ateuo
APPLICANT: Nakata, Ateuo
APPLICANT: Sinagawa, Hideo
APPLICANT: Sinagawa, Hideo
APPLICANT: Sairo, Ateuo
TITLE OF INVENTION: HIV ANTIGEN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE Birch, Stewart, Kolasch and Bir
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A
81.1%; Score 2818;
81.3%; Pred. No. 4e
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ACPKVSPEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG 242
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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,657
FILING DATE: 07-UN-1995
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/375,510
FILING DATE: 18-JAN-1995
APPLICATION NUMBER: US/07/985,949
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: SVERBEND: LECHING:
NAME: SVERBEND: LECHING:
REFERENCE/POCKET NUMBER: 30,330
REFERENCE/POCKET NUMBER: 310
TELECOMMUNICATION NUMBER: 310
TELECOMMUNICATION NUMBER: 310
                                                                                                                                                      APPLICANT: Saito, Atsushi
APPLICANT: Saito, Atsushi
APPLICANT: Sinagawa, Hideo
APPLICANT: Sinagawa, Hideo
APPLICANT: Nakata, Atsuo
APPLICANT: Nakata, Atsuo
APPLICANT: Nakata, Atsuo
APPLICANT: Nakata, Atsuo
AURESPONDENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virgini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  ; Sequence 2, Application US/08487657
; Patent No. 5834267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 826 amino acide
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703) 241-1300
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Best Local Similarity 82.9%;
Matches 540; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
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                                                                                                                                            US-08-487-657-2
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82.9%; Pred. No. 7.4e-224;
ive 34; Mismatches 56; Indels 21;
            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/985,949
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: SVENBSON, LEONARG R.
REGISTRATION NUMBER: 30,330
REGISTRATION NUMBER: 216-309P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                                                                         APPLICATION NUMBER: US/08/375,510
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
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US-08-375-510-2
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94 NIWWKNDWVEQWHEDIISLWDQSLKPCVKLTPLCVSLKCTDL--KNDTNTNSSSGRMIME- 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/09718096
| Patent No. 6589763
| Fatent No. 6589763
| Fatent No. 6589763
| GENERAL INFORMATION:
| APPLICANT: Von Laer, Meike-Dorothee
| TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV |
| FILE REFERENCE: 35-195 | CURRENT APPLICATION NUMBER: US/09/718,096 |
| CURRENT APPLICATION NUMBER: DE 19856463.5 |
| PRIOR PILING DATE: 1998-11-26 |
| PRIOR FILING DATE: 1999-11-25 |
| PRIOR FILING DATE: 1999-11-25 |
| PRIOR APPLICATION NUMBER: US 09/309,572 |
| PRIOR APPLICATION NUMBER: US 09/309,572 |
| PRIOR PILING DATE: 1999-11-25 |
| PRIOR PILING DATE: 1995-11-25 |
| PRIOR PILING DATE: 1999-11-25 |
| PRIOR PILING DATE: 1995-11-25 |
| PRIOR PILING DATE: 1999-11-25 |
| PRIOR PILING DATE: 1995-11-25 |
| PRIOR PI
                                                                                                                                  322 -GNMRQAHCNISRAKMNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEF
                                                                                                                                                                                                                                                                                                                                     63 NAWKNINMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    539 IKAQQHILIQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKT
       SLAEEEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRK--RVTLGPGRVWYTTGEI
                                 LGNIRQAHCNISRAQWNNTLQQIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEF
                                                                                                                                                                                                     FYCNSTOLFNSAWNTSNGTWSVTRKOKDTG-DIITLPCRIKQIINRWQVVGKAMYALPI
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                                                                                                                                                                                                                                                                                                                                                                                                     479 KAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLRA
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81.0%; Score 2814.5; DB 2;
Best Local Similarity 82.9%; Pred. No. 7.8e-224;
Matches 540; Conservative 34; Mismatches 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: envelope polyprotein US-09-718-096-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 854
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US-09-718-096-23
       243
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                                                                                                                                                                                   294 -GNWRQAHCNISRAKWNATLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEF
                                                                                                                                                                                                                                                                                                                                                                              410 SGQIRCSSNITGLLLTRDGGNNNNGSEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 LWVIVYYGVPVWKGATTTLFCASDAKAYDTEVHNWATHACVPTDPNPQEVVLVNVTENF
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                                                     SLAEEEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRK--RVTLGPGRVWYTTGEI
                                                                            LGNIRQAHCNISRAQWNNTLQQIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEF
                                                                                                                                                                                                                                                PYCNSTQLFNSAWNVTSNGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYALPI
                                                                                                                                                                                                                                                                                                 PYCHSTQLFNSTW---FNSTWSTEGSNNTEGSDTITLPCRIKQFINMWQEVGKAMYAPPI
                                                                                                                                                                                                                                                                                                                                                  KGLIRCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT
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APPLICANT: Heinrich-Pette-Institut
INFORMATION: Retroviral hybrid vectors pseudotyped with LCMV
INTE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
FILE REPERENCE: P50489
CURRENT PILING DATE: 199-06-11
EARLIER APPLICATION NUMBER: DE 198 56 463
EARLIER FILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDQIWNNMTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQLDKWASL 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: envelope polyprotein
US-09-309-572-23
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18-09-3109-572-23
Sequence 23, Application US/09309572
Patent No. 6440730
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                           SLAEEEVVIRSENFINNAKTIIVQLNVSVEINCTRPNNHTRK--RVTLGPGRVWYTTGEI 300
                                                                                                                                         FYCNSTQLFNSAWNVTSNGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYALPI 418
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                                          ACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG 261
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APPLICANT: Memphis, TN 38101-0318
APPLICANT: United States of America
APPLICANT: Coleciough, Christopher
APPLICANT: Coleciough, Christopher
APPLICANT: Slobod, Raren
TITLE OF INVENTION: PREPARATION AND USE OF VIRAL VECTORS FOR
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                          649
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ZIP: 07601

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                St. Jude Chidren's Research Hospital
332 No. 5846546th Lauderdale
PO Box 318
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Patent No. 5846546
GENERAL INFORMATION:
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STREET: 411 HACKENSACK AVENUE
CITY: HACKENSACK
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlmer
REGISTRATION UNDRER: 35,135
REFERENCE/DOCKET UNDRER: 1340
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: KLAUBER &
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APPLICANT:
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US-08-788-815-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 TSVITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGIRPVVST
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                                                                                                                                                                                   81.0%; Score 2814; DB 1;
82.1%; Pred. No. 8.9e-224;
ive 39; Mismatches 61;
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LENGTH: 880 amino acide
TYPE: amino acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: protein
                                                                                                                                                                                                                    Best Local Similarity 82.1
Matches 540; Conservative
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Job time : 69.9631 secs
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Best Local Similarity
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NGSLAEEEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEI
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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(cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*

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(cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
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US-10-780-507-121

US-10-780-507-121

US-10-780-507-121

US-10-780-507-121

US-10-190-435-29

US-10-90-438-29

US-10-90-438-2

US-10-90-438-2

US-10-90-438-2

US-10-90-438-2

US-10-90-438-2

US-10-976-619-2

US-10-976-619-2

US-10-976-619-2

US-10-976-619-2

US-10-976-912-28

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US-11-048-554-11
US-10-026-741-103
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Patent No. US20020155120A1
GENERAL INFORMATION:
APPLICANT: LOWell, George
APPLICANT: Vancott, Thomas
APPLICANT: Wancott, Thomas
TITLE OF INVENTION: INDUCING MUCOSAL IMMUNITY
CURRENT APPLICATION NUMBER: US/09/938,406
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1996-07-10
PRIOR FILING DATE: 1996-07-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTESEQ for Windows Version 4.0
IENGTH: 868
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                                                                                      US-09-966-931-32
US-10-459-121-32
US-10-196-515-3
US-11-048-554-3
US-11-048-554-3
US-11-048-554-12
US-11-048-554-12
US-11-048-554-12
US-10-325-468-15
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US-09-891-609-4
US-09-891-609-2
US-10-325-468-29
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US-10-780-993-17
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Best Local Similarity 100.
Matches 649; Conservative
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ORGANISM: Virus HIV-1
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Db 148 MEKGEIKNCSFNITTSIRDKVQKEYALFYKLDVVPIDNDNTTNNTTSYRLISCNTSVITQ 207 Qy 183 ACEKVSFEDIPHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG 242 Db 208 ACEKVSFEDIPHYCAPAGFAILKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG 267 Qy 243 SLAEEEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRAVWYTTGEILG 302 [540 KAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKTL 540 KAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKTL 566 EAQQHLLQLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLICTTAVPWNASWSNKSL 600 DQIWNNWTWMEWDREIDNYTHLIYTLIESSQNQQEKNQQELQLDKRASL 649	RESULT 3 US-10-441-226-2 i Sequence 2, Application US/10441926 i Sequence 2, Application US/10441926 i Publication No. US20040115621A1 i GENERAL INFORMATION: APPLICANT: Redigo, Allen APPLICANT: Mullins, James A. i APPLICANT: Mullins, James A. i APPLICANT: Mullins, James A. i TITLE OF INVENTION NUMBER: US/10/441,926 CURRENT PELING DATE: 2001-05-19 i FRIOR PILING DATE: 2000-02-18 i FRIOR PILING DATE: 2000-02-18 i RIOR PILING DATE:
301 IGNIROAHCNISRAQWINTLQQIATTLREQFGNKTIAFNQSSGGDPEIVWHSFNCGGEFF 360 333 IGNIROAHCNISRAQWINTLQQIATTLREQFGNKTIAFNQSSGGDPEIVWHSFNCGGEFF 392 361 YCNSTQLFNSAMNYTSNGTWSYTRXQXDTGDIITLDCRIKQIINRWQVVGKAMYALDIKG 420 393 YCNSTQLFNSAMNYTSNGTWSVTRXQXDTGDIITLDCRIKQIINRWQVVGKAMYALDIKG 420 421 LIRCSSNITGLLITRDGGGENQTTEIFFPGGDMRDNWRSELYKYKVVKIEPLGVAPTKA 480 421 LIRCSSNITGLLITRDGGGENQTTEIFFPGGDMRDNWRSELYKYKVVKIEPLGVAPTKA 512 481 KRRVVQREKRAVGMLGAMFLGFLGAAGSTWGATSMALTVQARQILSGIVQQQNNLLRAIK 540 [SULT 2 10-780-507-51 10-780-507-51 Subjuction US/10780507 Subjuction No. US20050137387A1 SENERAL INFORMATION: APPLICANT: WULLINS, James I. APPLICANT: RODRIGO, Allen G. APPLICANT: LEARN, Gerald H. APPLICANT: LEARN, Gerald H.	APPLICANT: NICKEL, David C. APPLICANT: NICKEL, David C. APPLICANT: ADRIEN, MARK A. TITLE OF INVESTION: ANGESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPORTED IN ANGESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPORTED: 2004-02-17 PRIOR RELING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: US 60/183,659 PRIOR FILING DATE: 2001-02-18 PRIOR FILING DATE: 2003-02-14 PRIOR FI

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               SGGGTWEGEKGEIKNCSFNVTTSIRDKWQKEYALFYKLDVVPIDNDNNYTNNNTSYRLIN 212
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                                                                                                                                                                                         CNTSVITQACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVV 234
                                                                                                                 STQLLLNGSLAEEEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVW 294
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; Publication No. US20040116684A1
; GENERAL INPORMATION:
; APPLICANT: ROGIGO, Allen
; APPLICANT: ROGIGO, Allen
; APPLICANT: ROGIGO, Allen
; APPLICANT: Mullins, James I.
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
; FILE REFERENCE: 08987-01201
; CURRENT APPLICATION NUMBER: US/10/441,949
; CURRENT FILING DATE: 2003-05-19
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2000-02-18
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FREESE for Windows Version 4.0
; SEQ ID NO 2.
; LEMGTH: 883
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US-10-441-949-2
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ORGANISM: Artificial Seguence
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Matches 564; Conservative
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APPLICANT: MULLINS, James I.
APPLICANT: RODRIGO, Allen G.
APPLICANT: RODRIGO, Allen G.
APPLICANT: LEARN, Gerald H.
APPLICANT: LIARN, Gerald H.
APPLICANT: LIARN, GERALD H.
APPLICANT: LIARN, GERALD H.
APPLICANT: LIARN, GERALD AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPORTING TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPORTING OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS APPLICATION NUMBER: US/10/780,507
CURRENT FILING DATE: 2004-02-17
PRIOR APPLICATION NUMBER: PCT/US01/05288
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-03-18
PRIOR FILING DATE: 2000-03-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn version 3.1
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US-10-780-507-121
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Best Local Similarity 84.7%; Pred. No. 6.5e-227;
Matches 564; Conservative 27; Mismatches 54;
              CURRENT APPLICATION NUMBER: US/10/780,507
CURRENT FILING DATE: 2004-02-17
PRIOR PLILING DATE: 2004-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR PILING DATE: 2010-02-16
PRIOR APPLICATION NUMBER: PCT/US01/05288
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2000-02-18
PRIOR PILING DATE: 2000-02-18
PRIOR FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PATENTIN VETBION 3.1
LENGTH: 883
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   FILE REFERENCE: 16336-001320US
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APPLICANT: RODRIGO, Allen G.
APPLICANT: LEARN, Gerald H.
APPLICANT: LI, Fusheng
APPLICANT: LI, Fusheng
APPLICANT: NICKLE, David C.
APPLICANT: JENSEN, Mark A.
TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOSENIC COMPO
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                                                                                                                               Length 883;
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                                                                             ; OTHER INFORMATION: Ancestral HIV-1 group M, subtype B, US-10-780-507-2
                                                                                                                        Query Match 85.7%; Score 2977.5; DB 5; Best Local Similarity 84.7%; Pred. No. 6.5e-227; Matches 564; Conservative 27; Mismatches 54;
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                                 TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                FINMWKNINWVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLRNVTNINNSSE-----
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505 KAKRRVVQREKRAVGIIGAMFLGFLGAAGSTMGAASMTLTVQARQLLSGIVQQQNNLLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 NLWYTVYYGVPVWKRATTTLFCASDAKAYDTEVHNVWATHACVFTDBNPQEVVLENVTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 EQRGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSVI
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                                        539 IKAQQHLLQLTVWGIKQLQARILAVBRYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NLWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENERATING TITLE OF INVENTION: AN IMMUNE RESPONSE.
FILE REFERENCE: 12804-005002
CURRENT APPLICATION NUMBER: US/10/093,953A
CURRENT FILING DATE: 2002-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/186,364
PRIOR APPLICATION NUMBER: US 60/186,364
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR PRILING DATE: 2001-03-02
PRIOR PRILING DATE: 2001-03-02
PRIOR PRILING DATE: 2001-09-25
PRIOR PRILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 29
                                                                                                                                                                                                                                                                     Sequence 29, Application US/10093953A Publication No. US20040105871A1
                                                                                                                                                                                                                                                                                                                              APPLICANT: Robinson, Harriet L. APPLICANT: Smith, James M. APPLICANT: Hua, Jian
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Amara, Rama
Wyatt, Linda
Earl, Patricia
                                                                                                                                                                                                                                                                                                                                                                                               Moss, Bernard
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                                                                                                             APPLICANT: MULLINS, James I.
APPLICANT: MULLINS, James I.
APPLICANT: RODRIGO, Allen G.
APPLICANT: LEARN, Gerald H.
APPLICANT: LEARN, Gerald H.
APPLICANT: LEARN, Gerald H.
APPLICANT: LI, Fusheng
APPLICANT: LI, Fusheng
APPLICANT: JERNSH, MARK A.
ITILE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPC
FILE REPERBUCE: 16336-001320US
CURRENT APPLICATION NUMBER: US/10/780,507
CURRENT APPLICATION NUMBER: US 10/204,204
PRIOR FILING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2000-02-18
PRIOR PELING DATE: 2000-02-18
PRIOR PELING DATE: 2003-02-14
PRIOR FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PATCHILING VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              common ancestor reconstruction of clade B gp 160 prot
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85.6%; Pred. No. 1.1e-224;
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                                                     Sequence 50, Application US/10780507; Publication No. US20050137387A1; GENERAL INFORMATION:
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OTHER INFORMATION: ein sequence
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ORGANISM: Artificial sequence
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Best Local S:
Matches 557
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243 SLAEEEVVIRSENFTWNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEILG 302
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                                                                                                                                                                                                                                                                                                                                                        543 RAIEAQQHLLQLTWGIKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTAVPWNASWSN
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                                                                                                                                                     NSTQLFNSAWNVT----SNGTWSVTRKQKDTGDITTLPCRIKQIINRWQVVGKAMYALP
                                                                                                                                                                                                                                           IKGLIRCSSNITGLLLTRDGGGE-NQTTBIFRPGGCDMRDNWRSELYKYKVVKIEPLGVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 ACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10241009
; Bedyence 2, Application US/10241009
; Publication No. US20030170614A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYPUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF;
; CURRENT APPLICATION NUMBER: US/10/241,009
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 83.3%; Pred. No. 1.7e-219;
Matches 544; Conservative 40; Mismatches 38;
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-10-241-009-2
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NGSLAEEEVVIRSSNFTDNAKNIIVQLKESVEINCTRPNNNTRKSIHIGPGRAFYTTGEI 317
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APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BARNETT, Susan W.
APPLICANT: ENGELBERECH, Susan
APPLICANT: ENGELBERECH; Susan
APPLICANT: VAN RENSBURG, Estrelita J.
ITILE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C;
ITILE OF INVENTION: POLYNETIDES, POLYPEPTIDES AND USES THEREOF;
ITILE OF INVENTION: POLYNETIDES, POLYPEPTIDES AND USES THEREOF;
ITILE OF INVENTION: POLYNETIDES, DOLYPEPTIDES AND USES THEREOF;
ITILE OF INVENTION NUMBER: US/10/190,435;
CURRENT APPLICATION NUMBER: US/20/12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PATENTIN VET. 2.0
; SEQ ID NO 2.
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83.3%; Pred. No. 1.7e-219;
Live 40; Mismatches 38; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDQIWNNMTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQLDKWASL
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US-10-190-435-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/10190435; Publication No. US20030143248A1; GENERAL INFORMATION:
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Best Local Similarity 83.3
Matches 544; Conservative
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TYPE: PRT
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| Bublication No. US20030198621A1
| GENERAL INFORMATION:
| APPLICANT: CAN MEGEDE, Jan |
| APPLICANT: LIAN, Ying |
| TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR |
| TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF |
| FILE REPERENCE: 2302-18702 / 18702.002 |
| CURRENT APPLICATION NUMBER: US/10/190,305A |
| CURRENT PILING DATE: 2002-07-05 |
| NUMBER OF SEQ ID NOS: 93 |
| SOFTWARE: PATENTIN VET: 2.0 |
| SEG ID NOS: 93 |
| SOFTWARE: PATENTIN VET: 2.0 |
| SEG ID NOS: 93 |
| SOFTWARE: PATENTIN VET: 2.0 |
| SEG ID NOS: 93 |
| SOFTWARE: PATENTIN VET: 2.0 |
| SEG ID NOS: 93 |
| SOFTWARE: PATENTIN VET: 2.0 |
| SEG ID NOS: 93 |
| SOFTWARE: PATENTIN VET: 2.0 |
| SEG ID NOS: 94 |
| SEG ID NOS: 95 |
| SEG ID 
                                                           484 PIKAKRRVVQREKRAV-TLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLL
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                                                                                                                                    363 NSTQLFNSAWNVT----SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYALP
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Matches 544; Conservative
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SLAEEGVVIRSENFTDNAKTIIVQLKESVEINCTRPNNNTRKSITIGPGRAFYATGDIIG
                                                                                                                                                                NSTQLFNSAWNVT----SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYALP
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APPLICANT: ZUR MEGEDE, Jan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BANNETT, SUBAN
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE FILTE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF FILE REFERENCE: 2300-1621.20
CURRENT APPLICATION NUMBER: US/10/190,434B
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO.2
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US-10-190-434B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.0%; Score 2883.5; DB 4; Length 83.3%; Pred. No. 1.7e-219;
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QY 303 NIROAHCRISRAQWINTLQQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGEFFYC 362 Db 317 DIRQHHCNISGEKWINTLKQIATTLREQFGNKTIVFKQSSGDPEIVWHSFNCGGEFFYC 376 QY 363 NSTOLFNSAWNYISNGTWSYTRKQKDTGDITLLCRIKQIINRWQVGKAMYALP 417 Db 377 NSTQLFNSAWNYISNGTWSYTRKQKDTGDITLLCRIKQIINRWQVGKAMYALP 423 QY 418 IKGLIRCSSNITGLLTRDGGE-NQTTEIFRPGGGDMEDNWRSELYKYKVVKIEPLGVA 483 QY 477 PTKAKRVVQREKRAVGHLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLL 536 Db 484 PTKAKRRVVQREKRAV-TLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLL 536 Db 537 RAIKAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSN 596 Db 543 RAIRAQQHLLQLTVWGIKQLQARVLLAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSN 602 QY 597 KTLDQIWNNATWMEWBEREIDNYTHLIYILESCQNQQEKQQELLQLDKWASL 649 Db 603 KSLDQIWNNATWMEWBEREIDNYTHLIYILESCQNQQEKQGLLGLDKWASL 655	RESULT 14 US-09-47-22 S-quence 2, Application US/09476242 S-quence 2. Application US/09476242 Patent No. US20020146683A1 GENERAL INPORMATION: APPLICANT: BARNETT, Susan APPLICANT: HARTOG, Karin TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES FILE REFERENCE: 1605.002 CURRENT APPLICATION NUMBER: US/09/476,242 CURRENT APPLICATION NUMBER: US/09/476,242 CURRENT APPLICATION NUMBER: US/09/476,242 MUMBER OF SEQ ID NOS: 26 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 CRENTH: 847 TYPE: PRT ORGANISM: Human immunodeficiency virus US-09-476-242-2 Query Match Best Local Similarity 83.0%; Score 2883.5; DB 3; Length 847; Best Local Similarity 83.3%; Pred: No. 1.7e-219; Matches 544; Conservative 40; Mismatches 38; Indels 31; Gaps 7;	Dy 123 RGKGBMRACSPUTLECASDAKAYDTEAHNWATHACVPTNPNPOGEVULENVTENP 62	Db 262 SIAEEGVVIRSENFTDINKTIIIVQLKESVEINCTRPNNNTRKSITIGFGRAFYATGDIIG 321 Qy 303 NIRQAHCNISRAQMNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGEFFYC 362 1
Qy 303 NIROAHCNISRAQMNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGEFFYC 362 Db 317 DIRQAHCNISGEKMNNTLQQIATKLQGGGRKTIVFKQSSGGDPEIVMHSFNCGGEFFYC 376 Qy 363 NSTQLFNSTRNNTLACQIATKLQAQFGNKTIVFKQSSGGDPEIVMHSFNCGGEFFYC 376 Db 377 NSTQLFNSTRNNTLACQIATKLQCGGNKTIVFRQSGGDRANTALP 417 A18 IKGLIRCSSNITGLLTRDGGGE-NQTTEIFRPGGGDRRDNWRSELYKYKVKYEDLGVA 476 Db 424 IRGQIRCSSNITGLLTRDGGGE-NQTTEIFRPGGGDRRDNWRSELYKYKVVKIEDLGVA 483 Qy 477 PTKAKRRVVQREKBAVGMLGAMFLGFLGAAGSTMGATSWALTVQARQLLSGIVQQQNNLL 536 Db 484 PTKAKRRVVQREKBAV-TLGAMFLGFLGAAGSTMGARSLTLTVQARQLLSGIVQQQNNLL 542 CQy 537 RAIKAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSN 596 Db 543 RAIKAQQHLLQLTVWGIKQLQARYLLAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSN 602 CQy 537 RAIKAQQHLLQLTVWGIKQLQARYLLAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSN 602 CQy 537 KTLDQIMNNMTWMEWBRREIDNYTHLIYTLIEBSQNQQEKNQGELGLGLGLGDKWASL 649 CD 603 KSLDQIWNNMTWMEWBRREIDNYTHLIYTLIEBSQNQQEKNQGELGLGLGLGLGCTAVPWASL 655	RESULT 13 US-10-976-619-2 Sequence 2, Application US/10976619 Publication No. US20050214256A1 GENERAL INFORMATION: APPLICANT: ZUR MEGEDE, Jan APPLICANT: LIAN, Ying TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B TITLE OF INVENTION: POLYNUCLEOTIDES POLYPEPTIDES AND USES THEREOF CURRENT APPLICATION NUMBER: US/10/976,619 CURRENT FILING DATE: 2004-10-29 PRIOR FILING DATE: 2004-10-29 PRIOR FILING DATE: 2002-09-06 NUMBER OF SEQ ID NOS: 68 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: FEATURE: OTHER INFORMATION: Description of Artificial Sequence: SF162	Query Match Bast Local Similarity Bast Similarity Bast Similarity Bast Local Similarity Bast State Sta	Db 197 ACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTNVSTVQCTHGIRPVVSTQLLLNG 256 Qy 243 SLAEBEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEILG 302

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                      ----ITLPCRIKQIINRWQEVGKAMYAPP
                                                      IKGLIRCSSNITGLLLTRDGGGE-NQTTEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVA
                                                                          PTKAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Berman, Phillip W.
APPLICANT: Berman, Gerald R.
NAKAMURA, Gerald R.
NUMBER OF INVENTION: HIV Envelope Polypeptides
OCRRESPONDENCE: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: MCCUtchen, Doyle, Brown & Ener
STREET: 3 Embarcadero Center
CITY: San Francisco
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83.0%; Pred. No. 5.5e-217;
iive 42; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966,931
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SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-966-931-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 38903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                           Sequence 28, Application US/09966931
Publication No. US20030064361A1
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Haliday, Emily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-393-2000
TELEFAX: 415-393-2286
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                    NSTOLFNSTWNNTIGPNNTNGT
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SEQUENCE CHARACTERISTICS:
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Best Local Similarity 83.0
Matches 537; Conservative
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                                                                      NIWWENNIWVEQWHEDIISLWDQSLKPCVKLTPLCVTLNCTDL--KNATNTISSS----WGK
                                                                                                                                                           LWVTVYYGVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEIGLENVTENF
                                            NAWKNNNVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTELSIIVVWEQ
                                                                                                                                 123 RGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSVITQ
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Job time : 212.547 secs
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Scoring table:

Minimum DB Maximum DB

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Publication No. US2005025512341

GREERAL INFORMATION:

APPLICANT: The Trustees of the University of Pennsylvania

APPLICANT: Medina, Maria Fe C.

APPLICANT: Mobines, Carry

TILLE OF INVENTION: Chimeric Ebola Virus Envelopes and Uses, Therefor

CURRENT PLING DATE: 2004-10-28

PRIOR PLICATION NUMBER: US 60/376,480

PRIOR PLILING DATE: 2002-04-30

PRIOR PLILING DATE: 2002-06-04

PRIOR PLILING DATE: 2002-06-04

PRIOR PLILING DATE: 2002-06-04

PRIOR PLILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Version 3.2

SEQ ID NOS: 67

SEQ ID NOS: 67
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38; Mismatches 56; Indels
                                               US-11-107-364-34
US-11-151-598-11
US-11-029-095A-2
US-11-029-095A-2
US-11-096-725-16
US-11-096-725-18
US-11-151-598-5
US-11-151-598-6
US-11-151-598-6
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Best Local Similarity 82.6*
Matches 538; Conservative
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Gaps

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Db 264 SLAEEEVVIRSVNFTDNAKTIIVQLNTSVEINCTRFNNNTRKIRIORGGRAFVTIGKI 323 Qy 301 LGNIRQAHCNISRAGWINTLQOIATTLREOFG-NKTIAFNOSSGGDBEIVWHSFNCGGEF 359 Db 324 -GNMRQAHCNISRAKWINTLKQIASKLREOFGNIKTIIFKQSSGGDBEIVWHSFNCGGEF 362 GV 360 FYCNSTQLFNSTAKWINTLKQIASKLREOFGNIKTIIFKQSSGGDBEIVWHSFNCGGEF 382 QY 419 KGLIRCSSNITGLLITROGGSNNTTEGSDTITLPCRIKQIINMWQKVGKAMYALPI 418	3 135-235-1 ence 1, Application US/11135235 ication No. US2006001935A1 RAL INFORMATION: LCCANT: Maraseco, Wayne LE OF INVENTION: Lentiviral Vectors and Us EREFERENCE: 2036-3027 RENT APPLICATION NUMBER: US/11/135,235 RENT APPLICATION NUMBER: 60/589,610 DR FILING DATE: 2004-07-21 DR FILING DATE: 2004-07-21 DR FILING DATE: 2004-07-21 DR FILING DATE: 2004-07-21 SEA OF SEQ ID NOS: 25 TWARE: Patentin version 3.2 NOTH: 856 PR: PR: PR: No	ധയ	3 LWYTYYYGVPVWKEATTILFCASDAKAYDTEANNYWATHACVPTDPNPQEVVLENYTEN 8	QY 63 NAWKANINVEQMHEDIISLMDQSLKPCVKLTPLCVTLACTDLNTNNTTNTTELSIIVVWEQ 122	OY 123 RGKGEMENCSFNITTSIRDKVQREYALFYKLDVEBIDDNKNTTNNTKYRLINCNTSVITQ 182	Qy 183 ACPKVSFEPIPIHYCTPTGPALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNG 242	OY 243 SIABEBUVIRSENFTNNAKTIIVQLAVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEI 300	Qy 301 LGNIRQAHCNISRAQWNNTLQQIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEF 359
264 SLAEEEVVIRSUNFTDNAKTIIVOLNTSVEINCTRPNNNTRKRIRIQRGDGRAFVTIGKI 323 301 LGNIRQAHCNISRAQWINTLQOIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEF 359 124 -GNMRQAHCNISRAQWINTLQOIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEF 359 1360 FYCNSTQLFNSAWNNTLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEF 382 1360 FYCNSTQLFNSAWNNTSNGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYARLPI 418 1383 FYCNSTQLFNSAWNNTSNGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYARLPI 418 11	325	Human immunodeficie 13 80.9%;	Matches 538; Conservative 38; Mismatches 56; Indels 19; Gaps 9;	3 LWVTVYSGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF 62 	63 NAWKANAVEQMHEDIISLWDQSLKPCVKLTPLCVTLACTDLATANTTHTTELSIIVVWEQ 122	123 RGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSVITQ 182 ::	183 ACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLILING 242 	243 SIAEEEVVIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRRRVTLGBGRVWYTTGEI 300

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539 IKAQQHLLQLTVWGIKQLQARILAVERYLKDQQLLGFWGCSGKLICTTAVPWNASWSNKT 598
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APPLICANT: TORIN, CLARISSE
APPLICANT: DELBERGUE, FREDERIC
TITLE OF INVENTION: RECOMBINANT MEASIES VIRUSES EXPRESSING EPITOPES OF
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TITLE OF INVENTION: ANTIGENS COMPOSITIONS
TITLE OF INVENTION: VACCINE COMPOSITIONS
TITLE OF INVENTION: VACCINE COMPOSITIONS
FILE REPREBRICE: 2356.0093
CURRENT APPLICATION NUMBER: DC7/EP03/07146
PRIOR APPLICATION NUMBER: EP 02291550.8
PRIOR PELING DATE: 2003-06-20
PRIOR PELING DATE: 2002-06-20
PRIOR PILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET: 3.3
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                      GQIRCSSNITGLLLTRDGGNSTETETEIFFRPGGGDMRDNWRSELYKYKVVRIEPIGVAPT
                                                                                                                                                                                                                                                                                            CNSTQLFNSAWNVT -- SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYALPIK
                                                                                                                                            386 CNTAQLFNSTWNVAGGTNGT------EGNDIITLQCRIKQIINMWQKVGKAMYAPPIT
                                                                                                                                                                                     GLIRCSSNITGLLLTRDGGGENQT-TEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT
                                                                                                                                                                                                                                                                 479 KAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLRA
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Publication No. US20060013826A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TANGY, FREDERIC
APPLICANT: TANGY, FREDERIC
APPLICANT: TORIN, CLARISSE
APPLICANT: DELEBECQUE, FREDERIC
TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES
TITLE OF INVENTION: ANTIGENS OF PROPOSITIONS
FILE REPERENCE: 2356.0033
CURRENT FILING DATE: 2003-06-20
PRIOR PELICATION NUMBER: FP 02291550.8
FROM PRIOR PLING DATE: 2003-06-20
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VOY: 3.3
SOFTWARE: PATENTIN VOY: 3.3
SOFTWARE: PATENTIN VOY: 3.3
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                                                                                                                                              SQIRCSSNITGLLLTRDGGNSNNESEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT
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                                       FYCNSTQLFNSAWNVTSNGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYALPI
                                                                  KGLIRCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRDNWRSELYKYKVVKIBPLGVAPT
                                                                                                                                                                                                KAKRRVVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLRA
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79.3%; Score 2756.5; DB 7; Length 681;
Best Local Similarity 79.4%; Pred. No. 2.6e-246;
Matches 517; Conservative 60; Mismatches 53; Indels 21;
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US-11-014-842A-25
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US-11-014-842A-25
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CNSTOLFNSAWNVT--SNGTWSVTRKOKDTGDIITLPCRIKQIINRWQVVGKAMYALPIK 419
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Sequence 31, Application US/11014842A

GENERAL INPORMATION:

APPLICANT: TAKNY: FREDERIC

APPLICANT: LORIN, CLARISSE

APPLICANT: DELBECQUE, FREDERIC

TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF

TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES

FILE REFERENCE: 2356.003

CURRENT APPLICATION NUMBER: PCT/PE03/07146

PRIOR APPLICATION NUMBER: PCT/PE03/07146

PRIOR PILING DATE: 2003-06-20

PRIOR FILING DATE: 2002-06-20

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 31

LENGTH: 857
                                                      GSLAEEEVVIRSENFINNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEIL 301
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                                                                        GNIROAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGEFFY
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Matches 507; Conservative
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                 KAKRRUVQREKRAVGMLGAMFLGFLGAAGSTMGATSMALTVQARQLLSGIVQQQNNLLRA 538
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                                                                                                                                                     GLIRCSSNITGLLITRDGGGENQT-TEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPT 478
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                                                                 GNIRQAHCNISRAQWNNTLQQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGEFFY 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.9%;
Matches 507; Conservative
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APPLICANT: TANGY.
APPLICANT: TANGY.
APPLICANT: TANGY.
APPLICANT: LORIN, CLARISSE
APPLICANT: LORIN, CLARISSE
APPLICANT: DELBERGOUG, FREDERIC
TITLE OF INVENTION: RECOMBINANT MEASIES VIRUSES EXPRESSING EPITOPES OF
TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
TITLE OF INVENTION: VACCINE COMPOSITIONS
FILE REFERENCE: 2356.0093
CURRENT FILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: PCT/EP03/07146
PRIOR APPLICATION NUMBER: EP 02291550.8
PRIOR APPLICATION NUMBER: EP 02291550.8
PRIOR APPLICATION NUMBER: PCT/EP03/07146
PRIOR APPLICATION NUMBER: POS: 43
SOFTWARE: Patentin Ver: 3.3
SOFTWARE: Patentin Ver: 3.3
                                                                                                                                                                                                                                                                                                  303 NIRQAHCNISRAQWANTLQQIATTLREQFGNKTIAFNQSSGGDPEIVMHSFNCGGEFFYC 362
                                                                                                                                        371 QIRCSSNITGLLITRDGGNSTETETEIFRPGGGDWRDNWRSELYKYKVVRIEPIGVAPTR
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                     RGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSVITQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 35, Application US/11014842A; Publication No. US20060013826A1; GENERAL INFORMATION:
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Matches 472, Conservative
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; Sequence 33, Application NO. US20066013826A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: MOLLET, LUCILE
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: WACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014,842A
; FRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2003-66-20
; PRIOR FILING DATE: 2002-06-20
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NOS: 43
; SEQ ID NO 33
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MMEEGEIKNCSFYITTSIRNKVKKEYALFNRLDVVPV---KN-TSNTKYRLISCNTSVIT
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ORGANISM: Human immunodeficiency virus type
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US-11-014-842A-33
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US-11-014-842A-33
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Sequence 37, Application US/11014842A

| Sequence 37, Application US/11014842A
| Publication No. US20060013826A1
| GENERAL INFORMATION:
| APPLICANT: TANGY, FREDERIC
| APPLICANT: LORIN, CLARISSE
| APPLICANT: MOLLET, LUCILE
| APPLICANT: MOLLET, LUCILE
| TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
| TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
| TITLE OF INVENTION: VACCINE COMPOSITIONS
| FILE REFERENCE: 2356.0093
| CURRENT APPLICATION NUMBER: US/11/014,842A
| FILE REPLICATION NUMBER: EP CT/EP03/07146
| PRIOR APPLICATION NUMBER: EP 02291550.8
| PRIOR FILING DATE: 2003-06-20
| PRIOR FILING DATE: 2002-06-20
| PRIOR SEQ ID NOS: 43
| SOFTWARE: PATENTIN Ver. 3.3
| SOFTWARE: PATENTIN Ver. 3.3
                    FINIMENDAMPEDIISLWDESLKPCVKLTPLCVTLECKNYTINTIN----NATSVTA 147
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Best Local Similarity
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CTYOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DFN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT APPLICATION NUMBER: DFJ/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR FILING DATE: 2003-06-27
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE FARENCE: FARENCE FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQIWNNMTWMEWDREIDNYTHLIYTLIEESQNQQEKNQQELLQLDKWASL 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 219, Application US/11022562; Publication No. US20050249742A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ruprecht, Ruth M.
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Publication No. US20060013826A1

GENERAL INFORMATION:

APPLICANT: TANGY: FREDERIC

APPLICANT: LORIN, CLARISSE

APPLICANT: LORIN, CLARISSE

APPLICANT: DELEBECQUE, FREDERIC

TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF

TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

FILE REFERENCE: 2356.093

CURRENT APPLICATION NUMBER: BC 1204-12-20

PRIOR FILING DATE: 2003-06-20

PRIOR PLILNG DATE: 2003-06-20

PRIOR PLILNG DATE: 2003-06-20

PRIOR APPLICATION NUMBER: EP 02291550.8

PROPURARE: PALENTIN VET. 3.3

SOFTWARE: PALENTIN VET. 3.3

SOFTWARE: PALENTIN VET. 3.3
                                                                                                                                                                                                                                          SLABEEVVIRSENFINNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEILG 302
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                                                                                                           RGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTTNNTKYRLINCNTSVITQ
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                                                                               NWW.KNNWVDQMHEDIISLWDESLKPCVKLTPLCVTL----
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Score 2421.5; DB 7; Length 789; Pred. No. 2.8e-215;

69.7**%**; 71.1**%**;

Query Match Best Local Similarity

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418
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                                                     LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF
  Gaps
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APPLICANT: Subject, Ruth M.

APPLICANT: Shieong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOCIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DFN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
FRIOR APPLICATION NUMBER: PCT/US03/20322
FRIOR APPLICATION NUMBER: 60/332718
FRIOR APPLICATION NUMBER: 60/332718
FRIOR APPLICATION NUMBER: 60/332718
FRIOR APPLICATION NUMBER: 60/332718
FRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOPTWARE: FRAUSE (FOR WINDOWS VERSION 4.0)
SEQ ID NOS: 340
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  Indels
  45;
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Pred. No. 7.2e-97;
                                                                                                                                                                               94 NYWKNNWYDQMHEDIISLWDESLKPCVKLTPLCVTL-
  44; Mismatches
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Conservative
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Best Local Similarity
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US-11-022-562-340
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309 GNKTVLPITLMSGLVFHSQ-PINTRPRQAWCRFG-GRWREAMQEVKQTLVQHPRYKGIND 366
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                                                                                                                         25 YVTVFYGIPAWKNASIPLFCA-----TKNRDTWGTIQCLPDNDDYQEIIL-NVTEAPD
                                                                                                                                                                                          4 WVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENFN
                                                                                                                                                                                                                                           TTELSIIVVWEQ------RGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPIDDN
                                                                                                                                                                                                                                                                                                                KNTTNNTKYRLINCNTSVITQACPKVSFEPIPIHYCTPTGFALLKCNDKKFNGTGP-CTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGATSMALTVQARQLLSGIVQQQNNLLRAIKAQQHLLQLTVWGIKQLQARILAVERYLKD
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                                                                     75;
                                   860;
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                                   DB 7; Length
                                                                     Indels
                                                                                                                                                                         64 MWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNTNTT
                                                                     247;
                                 32.0%; Score 1112.5; DB '38.8%; Pred. No. 2.4e-94; iive 92; Mismatches 247,
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ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite !
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/11084858; Publication No. US20050271678A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BRUST, Stefan
KNAPP, Stefan
GERKEN, Manfred
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                                                                     Conservative
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                                                 Local Similarity
les 263; Conserv
 JS-11-022-562-217
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                                                                                                                     TNDTARINLTARGGGDEVTFWTNCRGEFLYCKMNWFLN--WVEDRNTT---NQKPKEQ 424
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                                                                                                     NMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNC----TD------LNTNNTTN 110
                                                                                                                                                                       TT------BLSIIVVWEQ---RGKGEMRNCSFNITTSIRDKVQREYALFYKLDVEPI 158
                                                                                                                                                                                                     TTASAKVDMVNETSSCIAQDNCTGLEQEQMISCKFNMTGLKRDKKKEYNETWYSADL-VC 194
                                                                                                                                                                                                                                                              CSKVVVSSCTRMMETQTSTWFGFNGTRAENRTYLYWHGKDNRT---IISLNKYYNLTIKC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 GNKTIAFNOSS--GGDPEIVMHSFNCGGEFFYCNSTQLFNSAWNVTSNGTWSVTRKQKDT 389
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                                 62
                                                                 75
                                                                                                                                                                                                                                                                                                            CTNVSTVQCTHGIRPVVSTQLLLNGSLAEBEVVIRSENFTNNAKTIIVQLN--VSVEINC
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                                 LWVTVYYGVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLENVTENF
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 Gaps
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APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
TITLE OF INVENTION: 0.0450N
CURRENT PAPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2003-06-27
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
 64;
Mismatches 250; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Human Immunodeficiency Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 217, Application US/11022562 ; Publication No. US20050249742A1 ; GENERAL INFORMATION:
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102;
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EEAQIQOEKNMYELOKLNSW
264; Conservative
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LENGTH: 860
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/11/084,858
FILING DATE: 21-Mar-2005
CLASSIFICATION NUMBER: US/10/000,321
FILING DATE: 04-Dec-2001
APPLICATION NUMBER: US/10/000,321
FILING DATE: CURANOWN>
APPLICATION NUMBER: 09/131,551
FILING DATE: CURANOWN>
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERRANCE/DOCKET NUMBER: 58315/106/BEAK
TELEPHONE: (202) 672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-084-858-11
ZIP: 20007-5109
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514 SMALTVQARQLLSGIVQQQNNLLRAIKAQQHLLQLTVWGIKQLQARILAVERYLKDQQLL 573 574 GFWGCSGKLICTTAVPWNASWSNKTLDQIWNNMTWMEWDREIDNYTHLIYTLIEESQNQQ 633 62 GIWGCSGKLICTTAVPWNASWSNKSLEDIWDNMTWMQWEREIDNYTNTIYTLLEESQNQQ 121 2 SLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARVLAVGRYLRDQQLL 61 0; Gaps 4; Indels Query Match 18.8%; Score 653; DB 7; Best Local Similarity 87.5%; Pred. No. 5.2e-53; Matches 119; Conservative 13; Mismatches 4 d ò g

Length 145;

634 EKNQQELLQLDKWASL 649

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|||:||||:|||||| 122 EKNEQELLELDKWASL 137

7, 2006, 17:57:10 Search completed: March Job time : 25.8879 secs This Page Blank (uspto)